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Sequence 17, Application US/08162809

Patent No. 5457048

GENERAL INFORMATION:

APPLICANT: Pasquale, Elena B.

APPLICANT: Pasquale, Erecydoun G.

TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,

TOPRESSONDENCES: 26

CORRESPONDENCE ADDRESS:

ATREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STRATE: Galifornia

STRATE: Galifornia

STRATE: Galifornia

STRATE: Galifornia

STRATE: Galifornia

STRATE: Rependence Nometible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOUTHARE: PRECENTION NUMBER: US/08/162,809

FILING DATE:

ATTORNEY/AGENT TIRORAMATION:

NAME: Campbell, Cathryn A.

RECISTRATION NUMBER: 11,815

RECISTRATION NUMBER: 11,815

RECISTRATION NUMBER: 11,815

TELECOMMUNICATION NUMBER: 21,35-9001

TELERAX: (619) 535-9001

TELERAX
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                                                                                                                                                                                                                                                                         Score 14.8; DB 4; Length 3669;
Pred. No. 2.1e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2135 Adricarddaddarddcr 2152
              SOFTWARE: pt_FL_genes Version 2.0 SEQ ID NO 235 LENGTH: 3669
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1110 AGTTTATGGAGAGAGGCT 1093
                                                                                                                                                                                                                                                                                                                                                                                            3 AGTIBATGGAGAGTGGCT 20
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                              TYPE: DNA
CRANISM: Homo sapiens
FEATURE:
NAME/KEY:
LOCATION: (401)..(2806)
US-09-774-528-235
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; LOCATION: 10..
US-08-162-809-17
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APPLICANT: COHEN, CHARLES M.
TITLE OF INVENTION: NOVEL MORPHOGEN.RESPONSIVE SIGNAL
TITLE OF INVENTION: TRANSDUCER AND METHODS OF USE THEREOF
NUMBERS OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC.
STATE: 44 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZUPTER: 18 PC COMPATIBLE
COMPUTER READABLE FORM:
MEDIUM TYPE: PACHTON Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/727,118
FILING DATE: 08-OCT-1996
CLASSIFICATION NUMBER: 39,061
REFERENCE/DOCKET NUMBER: 39,061
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR EQUINO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3611 Dase pairs
TYPE: mucleic acid
STRANDENESS: single
TOPOLOGY: linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 14.8; DB 2; Length 3611; 88.9%; Pred. No. 2.1e+02; ive 0; Mismatches 2; Indels 0
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APPLICANT: Wang, Dunrui
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
FILE REFERENCE: 802
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CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
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Patent No. 6743619
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhao, Qing A.
Yang, Yonghong
Xue, Aidong U.
Wehrman, Tom
Wahman, Tom
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Matches 16; Conservative
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LOCATION: 905..1264
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US-09-774-528-235/c
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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RESULT 49
US-09-103-330-35
US-09-103-35. Application US/09103330A
Fatent No. 6319716
GENERAL INFORMATION
FAPPLICANT: TIKOO, SUREH K.
APPLICANT: TREDAY. FOLICE A.
TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
TITLE OF INVENTION: BOVINE ADENOVIRUS GENOME AND THEIR USE IN VACCINES
TITLE DEPENDENCE: 293102002121
CURRENT APPLICATION NUMBER: US/09/103,330A
CURRENT FILING DATE: 1998-06-23
FARLIER PELLING DATE: 1997-06-23
FARLIER PELLING DATE: 1997-06-23
FARLIER APPLICATION NUMBER: 08/164,292
FARLIER APPLICATION NUMBER: 08/164,292
MUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                              Gaps
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                                                                                              Query Match 74.0%; Score 14.8; DB 4; Length 4698; Best Local Similarity 88.9%; Pred. No. 2.2e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 14.8; DB 4; Length 5749;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                               RESULT 48

US-09-262-537-48

US-09-262-537-48

Sequence 48, Application US/09262537

Patent No. 64 79256

GENERAL INFORMATION:

APPLICANT Hayflick, Joel

TILE OF INVENTION: Lectomedin Materials and Methods

FILE REFERENCE: 27866/35307

CURRENT APPLICATION NUMBER: US/09/262,537

CURRENT FILING DATE: 1999-03-04

EARLIER PILING DATE: 1999-03-04

MUNBER OF SEQ ID NOS: 64

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Bovine adenovirus type 3 US-09-103-330-35
                                                                                                                                                                                                                                2109 AGTTCATGGAGAATGGCT 2126
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                                                                                                                                                                                       3 AGTTAATGGAGAGTGGCT 20
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88.9%;
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Best Local Similarity 88.9°
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
; ORGANISM: Homo sapiens
US-09-262-537-48
  NAME/KEY: unsure
                            ; LOCATION: (3921)
US-09-895-652A-1
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SEQ ID NO 35
FWGTH: 34446
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LENGTH: 5749
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APPLICANT: Macina, Roberta
APPLICANT: Macina, Roberta
APPLICANT: Macina, Regewari
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and
TITLE OF INVENTION: Treating Colon Cancer
TITLE DF INVENTION: Treating Colon Cancer
FILE REPERENCE: DEX-0211
FILE REPERENCE: DEX-0211
CURRENT APPLICATION NUMBER: 00/214,515
PRIOR PILITAG DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver: 2.1
LENGTH: 4698
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                                                                                  APPLICANT: Pasquale, Elena B.
APPLICANT: Sajiadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 74.0%; Score 14.8; DB 1; Best Local Similarity 88.9%; Pred. No. 2.1e+02; Matches 16; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDRER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELECHONE: (619) 535-9001
INFORMATION FOR SEQ 1D NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    California
: United States of America
US-08-162-809-11
; Sequence 11, Application US/08162809
Partent No. 5457048
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09895652A
Patent No. 6774223
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                           San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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US-08-162-809-11
                                                                                                                                                                                                                                                                                               STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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RESULT 50

US-08-375-709-1/C

US-08-375-709-1/C

US-08-375-709-1/C

Sequence 1, Application US/08375709

PATENT No. 5653898

PATENT NO. 5653898

PATENT NO. 1722

CONNTY: Washington

CONPUTER READALE FORM:

MUMBER OF SECTION NO. 1722

CONPUTER NO. 1722

CONPUTER NO. 1722

PATENT NO. 1722

PATENT
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Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Shewanella putrefaciens SCRC-2874 (FERM )
ORGANISM: BP-1625)
US-08-375-709-1
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3 AGTTAATGGAGAGTGGCT 20

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Search completed: December 3, 2004, 05:52:51 Job time: 104.316 secs

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B2224094 CH2 AG169335 Pan BZ164877 CH2 BX169283 Dan BX169508 Dan CB684683 OSU AW080408 xe5 AW080408 Xe5 CM10935 Rt CR10935 Rt	BE641809 MR1-SNO CR477607 CR477607 BF642242 CM3-EV0- BF521948 UI-R-Y0- AIS9464 WX78h12. H37761 VP46603.F1 W42610 ZC23408.F1 BF642969 UI-R-Y0- N33486 YY42f09.S1 AIS93323 tq43f08.	W42606 zc23d08.s1 BE349791 hq43b08.x R55760 yg89670.s1 CN388155 170005313 CK100560 C050P42.5 AA350346 EST57669 AA4486245 zv24902.s AA448624 sz24902.s AA64828 m522h06.s H99886 yx37h05.s1 CD539657 B0215807-AM217984 EST296699 AIIT04017 EST248649 AW917901 EST349205 AW917901 EST349205 AW917901 EST349205 AW917901 EST349205 AW917901 EST349205 AW917901 EST349205 AW19206 AH10606.x BI289988 UI-R-DKO-CC542271 B0242A05-AM918065 K-EST008-AM918065 K-EST008-AM918060 CUR-Y0-AM918060 CUR-Y0	AW389529 CM4-ST016 BES67119 601341289 CO644824 ILLUMIGEN EB294519 601173467 AZ017711 RFCI-23-2 CD542400 BO24A011. BI303830 UJ-R-DS0-2 AQ036740 CIT-HSP-2 BI291703 UJ-R-DM0-	NASO41 yx89506.51  NA72871 AV772871  BE29626 BR829375 MR1.HN006  CR147584 K.ESTO203  CR081886 FOLWARG S  CR081886 FOLWARG S  CR081886 FOLWARG S  CR176890 FOLWARG S  BE513527 601315037  BE513527 601315037  BE51469 FOLWARG S  BE51456 60107643  BG26026 602071373  CR388144 170005329  BR54059 60107643  BG26026 FOLWARG S  CR440796 UI.H-DII-AW957365 EST36555  CR440796 UI.H-DII-AW957365 EST36855  CR155728 K.EST0214  CR040699 Ligr-gss-AM040597  CR040699 Ligr-gss-AM040597  CR044099 Ligr-gss-AM040597  CR044099 Ligr-gss-AM040597  CR044099 Ligr-gss-AM040597  CR044139 UI.H-EII-BII-BII-BII-BII-BII-BII-BII-BII-BII
	BE84180 CR47760 CR47760 BF84924 BF52194 A195404 H37761 W42610 BF54296 N334296	M42606 BE34979 RE34970 CX10056 AA35034 AA435034 AA435034 AA435034 AA35034 AA35034 AA31790 AW21790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790 AW91790	AW38952 BE56711 CO64482 BE29451 AZ01771 AZ01771 AZ0383 AQ03674	1 AV772871 2 BF829375 6 CB147584 7 CR081886 7 CR081886 9 CR081886 9 CR081886 1 CR081886 1 CR081886 1 CR081886 1 CR081886 1 CR176891 2 BF87429 2 BF87429 2 BF87429 6 CR15589 6 CR15589 6 CR15589 6 CR15589 9 CR014089 1 AL040597 9 CR0447139 6 CA447139
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(Dases I to 338)

Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,

Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,

Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,

Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,

Magulre, L., Kennedy, S., Waterston, R. and Wilson, R.

Washu Hydra EST Project

Unpublished (2002)
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Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Putative full length read
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Hydra magnipapillata
Eukaryota; Metazoa, Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
                      resistant electrocompetent cells"
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Site_2: EcoRI"
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WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
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llarity 94.7%; Pred. No. 5.2e+02;
Conservative 0; Mismatches 1;
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94.7%; Pred. No. 4.7e+02;
ive 0; Mismatches 1;
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Location/Qualifiers
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Matches 18;
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AUTHORS
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Bukaryota; Matara; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;

Hydridae; Hydra.

Bose Hydra.

S Bode, H., Nguyen, Q.,

Martinaz, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,

Hiller, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R.,

Magnire, L., Kennedy, S., Waterston, R. and Wilson, R.

WashU Hydra EST Project

Unpublished (2002)

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Hyd Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
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1117020E1
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AGENCOURT
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Library.was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
                                                                                                                                                                                      BE032166 BE032342 BE0323612 BE0323613 BE0323613 BE032614 BE032690 BE032600 
                                                                                                                                                                  BF754317
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Seq primer: degenerate primer
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                                                                                                                                                                                      BE037166
BG922942
                                                                                                                                                                                                                                                                                                                                   BU326900
CN716357
CF894640
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CK768062
                                                                                                                                                                                                                                      BU339613
CN718964
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CB015299
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High quality sequence stop: 1.
Location/Qualifiers
                                                                        BU922006
                                                                                                                   BF723489
                                                                                                                                                                                                                                                                                      BY724318
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                                                                                                                                                                  BF754317
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CN633741.1 GI:47144818
EST.
RESULT 1
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JOURNAL
COMMENT
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REFERENCE AUTHORS ö

Gaps

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Indels

FEATURES

Length 338;

(+); Site 1: Not1;

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EST 13-JUN-2000
Martinez,D., Kibler,D., Hampson,S., Clifton,S., Pape,D., Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Ronko,I., Tsagareishvili,R., Maguire,L., Kennedy,S., Waterston,R. and Wilson,R. WashU Hydra EST Project Umpublished (2002)
Other ESTS: taf55b05.x1
Contact: Hans Bode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....(bases 1 to 427)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library was constructed by Thomas Holstein / Molecular Cell
Library materials provided by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (hrbode@uci.edu)
Putative full length read
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UI-R-BO1-age-d-07-0-UI.SI UI-R-BO1 Rattus norvegicus CDNA clone
UI-R-BO1-age-d-07-0-UI 3', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
University of Iowa
University of Iowa
Tel: 319 335 8250
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 9565
Fax: 319 335 966
Fax: 319 336 966
Fax: 319 336 966
Fax: 319 337 9667
Fax: 319 338 9667
Fax: 319 338 9667
Fax: 319 338 9667
Fax: 319 338 9667
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WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/coganism="Hydra magnipapillata"

/mol type=mmRNA"

/strain="sf-1 mutant of strain 105"

/db_xref="texon:608x EC100 (Epicentre), Tl Phage

resistant electrocompetent cells"

/clone lib="Hydra EST Darmstadt I"

/clone lib="Hydra EST Darmstadt I"

/site_1: Bluescript II SK (+); Site_1: Not1;

Site_2: ECORI"
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BE102024.1 GI:8494122
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Best Local Similarity 94.,
Best Local 8, Conservative
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BE102024
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                                                                                   CN772025 357 bp mRNA linear EST 20-MAY-2004 tad94d07.yl Hydra EST Darmstadt I Hydra magnipapillata cDNA 5' similar to TR:Q9VAKO Q9VAKO CG7568 PROTEIN: ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library was constructed by Corina Guder / GATC Konstanz, Germany Library was constructed by Corina Guder / GATC Konstanz, Germany Library materials provided by Thomas Holstein / Molecular Cell Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Putative full length read
Putative full length is
Seq primer: -40UP
High quality sequence stop: 357.
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Bode,H., Blumberg,B., Steele,R., Wigge,P., Gee,L., Nguyen,Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hydra magnipapillata"
/organism="Hydra magnipapillata"
/mol_type="mRNa"
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/clone lib="Hydra EST Darmstadt I"
/clone lib="Hydra EST Darmstadt II"
/clone lib="Hydra EST Darmstadt II"
/site_2: ECGII"
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Hydra magnipapillata
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
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Hydra magnipapillata
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: est@watson.wustl.edu
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CN634000
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Indels
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Pred. No. 5.4e+02;
0; Mismatches 1;
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/db_xref="ATCC (inhost):2034859"
/db_xref="taxon:10118"
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/organism="Rattus sp."
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Best Local Similarity 94.7%;
Matches 18; Conservative C
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Unpublished (1998)
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Rattus sp.
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Hydra magnipapillata

Hydra magnipapillata

Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;

Hydridae; Hydra.

1 (Dases 1 to 435)

8 Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,

Martinez, D., Kibbler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,

Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tasgareishvili, R.,

Magulre, L., Kennedy, S., Waterston, R. and Wilson, R.

Unpublished (2002)

Other ESTs: taeo6602.yl
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strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA Library Preparation. Soares Lab Clone distribution: clones will be available through Seq primer: M13 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library was constructed by Corina Guder / GATC Konstanz, Germany
Library materials provided by Thomas Holstein / Molecular Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tae06d02.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNa 3' similar to TR:Q9VAKO Q9VAKO CG7568 PROTEIN. ;, mkNA sequence. CN772716
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.0%; Score 17.4; DB 2;
llarity 94.7%; Pred. No. 5.4e+02;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                      organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    435 bp
                                                                                                                                      location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CAGTTAATGGAGAGTGGCT
                                                                                                                                                      .427
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Local Simi
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DEFINITION
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CN772716/c
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Matches
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Seq primer: degenerate primer
High quality sequence scop: 407.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REST) Catalog & Rat
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/note="Organ: spleen; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                resistant electrocompetent cells"

'clone lib="Hydra EST Darmstadt I"

/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: ECORI"
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/mol_type="mRNA"
/asrain="s2-1 mutant of strain 105"
/db xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre), T1 Phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 436)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
TTel: (301)-838-3529
Pax: (301)-838-0208
Email: nhlee@tigr.org
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Hydra magnipapillata
Hydra magnipapillata
Hydra magnipapillata
Bukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydrade; Hydra.

1 (bases 1 to 540)
SS Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
Hiller, L., Martin, J., Mylie, T., Dante, M., Theising, B., Bowers, Y.,
Gibbons, M., Stiter, E., Bennett, J., Ronko, I., Tsagareishvili, R.,
Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
Unpublished (2002)
Other EsTs: taf7lad6, yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU Hydra EST Project
WashU Hydra EST Project
WashU Hydra EST Project
WashU Hydra EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library was constructed by Thomas Holstein / Molecular Cell
Biology, TUD, Darmstadt DNA Sequencing by: Washington University
Genome Sequencing Center For information on obtaining a clone
please contact: Hans Bode (Eurbode@uci.edu)
Seq primer: degenerate primer
High quality sequence etcp: 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             540 bp mRNA linear EST 20-MAY-2004 taf71a06.x1 Hydra EST Darmstadt I Hydra magnipapillata cDNA 3' similar to TR:Q9VAKO Q9VAKO CG7568 PROTEIN. ;, mRNA sequence. CN777963. GENTY GENT
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/mol_type="mRNA"
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/mol_type="mRNA"
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/dol_host="TransforMax EC100 (Epicentre), T1 Phage
resistant electrocompetent cells"
/clone lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: ECORI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 94.7%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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KEYWORDS
SOURCE
ORGANISM
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CN777963/c
LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydra magnipapillata
Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.

(bases 1 to 517)
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, O.,
Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
Hillier, L., Martin, J., Wylle, T., Dante, M., Theleing, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tasgareishvili, R.,
Washu Hydra EST Project
Unpublished (2002)
                                                       CB736658 462 bp mRNA linear EST 11-APR-2003 AMGNNUC:MRBE3-00050-A4-A rat brain E15 (10374) Rattus norvegicus cDNA clone mrbe3-00050-a4 5', mRNA sequence.
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One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00050 row: a column: 4.
Location/Qualifiers

l. 462

/organism="Rattus norvegicus"
/mol_type="mRAM"
/db_type="mRAM"
/db_type="mRAM"
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/clone="mrbe3-00050-a4"
/fissue type="brain E15"
/clone Tib="rat brain E15"
/note="Vector: PBCB; Site_1: BstXI; Site_2: Not1; rat brain E15"
                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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WashU Hydra BST Project
WashI Harkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library was constructed by Corina Guder / GATC Konstanz, Germany
Library was constructed by Thomas Holstein / Molecular Cell
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                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
1 (bases 1 to 462)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 CAGTTACTGGAGAGTGGCT 116
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Best Local Similarity 94.7
Matches 18; Conservative
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RESULT 8
CB736658
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CN553187/c
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Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
Seq primar: degenerate primer.
High quality sequence stop: 515.

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Gaps

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Gaps

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ORIGIN

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CB613159
AMGNNUC:NRHY7-00021-G9-A nrhy7 (10850) Rattus norvegicus CDNA clone nrhy7-00021-G9 5', mRNA sequence.
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UI-R-BO1-aiy-f-05-0-UI.rl UI-R-BO1 Rattus norvegicus cDNA clone
UI-R-BO1-aiy-f-05-0-UI.s', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .557

/organism="Rattus norvegicus"

/organism="Rattus norvegicus"

/db_xref="texon.10116"

/clone="nrhy7-00021-g9"

/clone lib="nrhy7 (10850)"

/note="vector: pSPORT1; Site_1: Sall; Site_2: Not1; W Ratthypothalamus adult female Wistar rat avg. insert size 2.3 kb fraction 6 and 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
      Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.0%; Score 17.4; DB 6; Length 557; larity 94.7%; Pred. No. 5.6e+02; Conservative 0; Mismatches 1; Indels
                                                          Indels
Score 17.4; DB 2;
Pred. No. 5.6e+02;
0; Mismatches 1;
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97044477
8889548
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Plate: 00021 row: g column: 9.
Location/Qualifiers
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Rattus norvegicus
                                                                                                                                                  370 CAGTTACTGGAGAGTGGCT 388
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                                                                                                                 20
Match
Local Similarity 94.7%; Pries 18; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Dan Fitzpatrick
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1 (bases 1 to 557)
Amgen EST Program.
Amgen Rat EST Program
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                                                                                                                 2 CAGTTAATGGAGAGTGGCT
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BF563085/c
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/ Woll type="matk"

/ Strain="Sprague-Dawley"

/ de_xref="Laxon:10116"

/ dev_stage="adult"

/ de
                                                                                                                                                                                                                                                                                                                                            AW526046 Innear EST 06-MAR-2000 UI-R-BO1-aiy-f-05-0-UI.SI UI-R-BO1 Rattus norvegicus CDNA clone UI-R-BO1-aiy-f-05-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Easi: 13.3.35.9.50
Easi: 13.3.9.50
The sequence contained an oligo-dT track that was present in the oligouchiectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Notl site and the oligo-dT track served to identify it as a clone from the normalized medulla library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 9565
                     Score 17.4; DB 7; Length 540;
Pred. No. 5.6e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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Rattus norvegicus
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                                                                                                                                      2 CAGTTAATGGAGAGTGGCT 20
                     87.0%;
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                                                   Best Local Similarity 94.7
Matches 18; Conservative
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Ignomea nil (Japanese morning glory)

EST.

Ipomoea nil (Japanese morning glory)

ENARYOPATA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Denaryophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Convolvulaceae; Ipomoeae.

I (bases 1 to 705)

Strongaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Ilda,S. Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Ilda,S. Ontact: Tadasu Shin-i

Contact: 
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Ipomoea nil
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
/cultivar="Tokyo-kokei standard"
/db_xref="taxon:35883"
/dlone="jm38c04"
/tiscue type="mixture of flower and flower bud"
/clone_lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA linear EST 18-DEC-20 flower and flower bud Ipomoea nil
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87.0%; Score 17.4; DB 4; Length 705;
Best Local Similarity 94.7%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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Best Local Similarity 94.7%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 1;
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BJ572384/c
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BJ577489
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamidas Solanales; Convolvulaceae; Ipomoeae. I pomoeae. 1 to 673)

Experimental to 673; Shinozaki, K., Hayashizaki, Y., Kohara, Y., and Iida, S. Ests of Japanese morning glory

Inpublished (2002)

Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: To Genetic Resource Information
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-55-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism "Rattus norvegicus"
/organism "Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/dow stage="adult"
/lab_host="bline" [Life Technologies]"
/lab_host="bline" [Life Technologies]"
/lone="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a mixture
of the following tissues: thalamus, cerebellum,
/nypothalamus, medulla, pons, midbrain, cerebellum,
/nypothalamus, medulla, pons, midbrain, cerebellum,
/orpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest-eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
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BJ578386 Ipomoea nil mixture of flower and flower bud Ipomoea nil
EJ578386
                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
175 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 8256
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Enail: bento-soares@uiowa.edu
Enail: bento-soares@uiowa.edu
Enail: bento-soares@uiowa.edu
This clone will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LINL (info@niege-IIII.gov). IMAGE ID= 1797847
Seq primer: MJ3 Forward.
Seq primer: MJ3 Forward.
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Ipomoea nil (Japanese morning glory)
Ipomoea nil
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/mol_type="mRNA"
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BJ578386/c
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Genome Res. 6 (9), 791-806 (1996)
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         1 GCAGTTAATGGAGAGTGGC 19
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1 (bases 1 to 744)

S Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,T., Nitasaka,B., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S. ESTS of Japanes morning glory
Unpublished (2002)

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Tel: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  'tissue type="mixture of flower and flower bud" 'clone_lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /olone="jmi9k20"
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/clone_lib="Ipomoea nil mixture of flower and flower bud"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 bp mRNA linear EST 18-DEC-200
BJ572099 Ipomoea nil mixture of flower and flower bud Ipomoea nil
CDNA clone jm19k20 3', mRNA sequence.
asterids; lamiids; Solanales; Convolvulaceae; Ipomoeeae; Ipomoea.
              aberitable amiliary obtainates; convolutances; thousese, thousese, thousese, thouses in the 740)
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,?
Hoshino,A., Seki,M., Shin-i,T., Carninci,P., Kamiya,A., Shiraki,?
Nitasaka,E., Shinozaki,K., Hayashizaki,Y., Kohara,Y. and Iida,S.
ESTS of Japanese morning glory
Unpublished (2002)
Contact: Tadasus Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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                                                                                                                                                                                                                                                                                                            1. 740
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/mol type="mRXNA"
/cultivar="Tokyo-kokei standard"
/db xref="taxon:35883"
/clone="jm20i17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mmNA"
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/db_xref="texon:35883"
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                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Location/Qualifiers
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Best Local Similarity 94.7%;
Matches 18; Conservative (
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Best Local Similarity
Matches 18; Conserv
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/db_xref="traxon:lolif" / db_xref="traxon:lolif" / db_xref="traxon:lolif" / ddo_xref="traxon:lolif" / ddo_xref="traxon:lol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of lowa (156 MEBR, lowa City, IA 52242, USA Tel: 319 335 825 MEBR, lowa City, IA 52242, USA Tel: 319 335 825 MEMBR, lowa City, IA 52242, USA Tel: 319 335 826 MEMBR, lowaled the same sequence contained an oligo-dr track that was present in the Oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to verify it as a clone from the normalized distal colon library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seg primer: M3 Forward
BQ204219 746 bp mRNA linear EST 02-MAY-2002 UI-R-DN1-cmv-p-03-0-UI.SI UI-R-DN1 Rattus norvegicus cDNA clone UI-R-DN1-cmv-p-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 746)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
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TAG TISSURE-distal colon
TAG LIBEUT-R-DN1
TAG_EEQ-GAAGTGCTC"
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/strain="Sprague-Dawley"
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Viridiplantae; Streptophyta; Eukaryota, Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; I (bases 1 to 775)

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Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Siraki, M., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Contact: Tadasu Shin-i

Tadasu Shin-i

Institute of Genetics
Illi Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.
Hoshino, A., Seki, M., Shin-i, T., Carninci, P., Kamiya, A., Shiraki, T., Nitasaka, E., Shinozaki, K., Hayashizaki, Y., Kohara, Y. and Iida, S. Ests of Japanese morning glory Unpublished (2002) Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics National Institute of Genetics Till Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 10-559-81-6856
                                                                                                                                                                                                                                                                                                                       /organism="Ipomoea nil"
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/db_xxef="taxon:35883"
/db_xxef="taxon:35883"
/db_xxef="taxon:35883"
/db_xxef="taxon:35883"
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Best Local Similarity 94.7%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels
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/mol_type="mENA"
/culfiva="mENA"
/culfiva="Tokyo-kokei standard"
/db xref="taxon:35883"
/clone="jm8k23"
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BJ570485/c
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1 (Dases 1 to 754)

1 (Dases 1 to 754)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 Office of Gancer Genomics

4 Notional Cancer Institute, NIH

8 Idg. 31 RM10A07 Bethesda, MD 20892

5 Email: Gapbs-r@mail.mih.gov

7 Issue Procurement: Dr. 1gor Dawid

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bisocience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

High quality sequence stop: 679.

Location/Qualifiers

Senation/Qualifiers
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BJ570457.1 GI:27252285
BSF.
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/clone lib="NIGHD XGC_Sp1"
/note="Cogan: spleen; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.4 kb. Constructed by Life
Technologies."
                                                                                                                                           754 bp mRNA linear EST 14.
AGENCOURT 15207692 NICHD XGC_Sp1 Xenopus laevis cDNA clone
CRAGE::506637 5', mRNA sequence.
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Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
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            CAGTTACTGGAGAGTGGCT 389
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CF283555.1 GI:33643334
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BJ570457/c
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Gaps

GCAGTTGATGGAGAGTGGC 267

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1...1091
| organism="Triticum aestivum" |
| organism="Triticum aestivum" |
| db_xref="mRNA" |
| db_xref="mRNA" |
| /db_xref="mRNA" |
| /clone llb="Triticum and leaf; Vector: pCMV.SPORT6;
| /clone for growth: Seeds were germinated in a water-saturated mix (50% black earth and 50% ProMix) in a growth chamber for 7 days under an irradiance of 200 mmol or sec-1. The temperature was maintained at 20 degrees C with a 15-hr photoperiod under a relative humidity of 70%. After this period watering of plants was stopped. Four time points were sampled during a two week period; the first effer willing was observed and the last, two weeks later, consisted of live crown and leaf tissue (leaf tissue that was yellow was not included in sampled material). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [37,799].
Plate: Location/Qualifiers
                                                             mRNA linear EST 05-DEC-2003
Library 4 Gate 8 Triticum
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                                                                                                                                                                                                                                                             Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

1 (bases 1 to 1091)

4 Alaad,F., Crospy,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D., Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,

Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,

Penniker,C., Roach,J.L. and Sarhan,F.

Functional Genola Crops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatcon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769 Fax: 306 966 2033
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87.0%; Score 17.4; DB 7; Length 1091;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0.
                                                         CK163790 1091 bp
FGAS016424 Triticum aestivum FGAS:
                                                                                                                                                                                                                                          Triticum aestivum (bread wheat)
                                                                                                                   aestivum cDNA, mRNA sequence.
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Contact: Wm L Crosby
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AG612934/c
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Gaps

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Hattori, M., Toyda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Brattori, M., Toyda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattoriegsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC
Tsukuba are derived from the mouse BAC library MSMg01. For BAC
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Liver regeneration after PH
Unpublished

2 Chases 1 to 3276)
Xu, C.S., Li, W.Q., Li, Y.C., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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BAC end Sequences of Library MSMg01
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llarity 94.7%; Pred. No. 6.7e+02;
Conservative 0; Mismatches 1; Indels 0
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/clone_lib="MSMg01 Mouse Male BAC Library"
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Rattus norvegicus Cc2-27 mRNA, complete cds.
AY325247
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/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="w&Mg01-548K03.TJ"
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                                                                   Mus musculus molossinus
Mus musculus molossinus
                       AG612934.1 GI:48373764
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: EcoRI
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IALIGLAVWGQNILLDNMUDHERVVCARNRTVSKVDDFLAKGAKGTKNIGAKSLKDWAS
KIKKPRRVILLWKAGQAVDDFIEKLYCLDATGDIIIDGGNS ETRDTTRRCQDLKAKGI
LFUGSGQYSGGEBGARYGGSKERAKSLSQUYBEYGDIIAAKVGTGEPCCDMASSGLP
FDECTAGERTIJMSQUKLGCREPIKLKSLSQUYBEYGDIIAAKVGTGEPCCDMASSGLP
FDECTAGERTIJMSQUKLGCEPLIKSLSQUYPEYDGIIILTRODIIAAKVGTGELLEKIR
DSGAGKGTGKWTAISALEYGMYTLIGGAPRECHTLINYGCHGARGKERCLEKIR
DSGAGKGTGKWTAISALEYGMYTLIGARONDCQDSWRRVISTINYGCHGARGKGREETEBER
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BEBEBEBEBEBEBEBEBERKKKKKKKKKKKKKRKVRRVERESRRYYALLEGLSAVWBE
VBAEBQQQYSHRQRLKAAVHYTVGCLCQEVELDKQVHLSKQTIAAISEVTERQCENFA
KOLRHENLPANIJQAQDPIGAHTYBELSKCKKKKREVVERESRRYYALLEGLSAVWBE
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KOLBSYTEDSYTEDSYGTDSYGYTEDSYGYTEDSYGYTEDSYGITEDSYG
VTEDSYTEDSYTEDSYGTEDSYGYTEDSYGYTEDSYGYTEDSYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MDOXTPEANSRASSPCOEFECFOIIPTVETPYLARAGKNEFLNL
VPDIEEVRAGSVVSKKGYLHFKEPLSSNWAKHFVVVRRPYVFIYNSDKDPVERGIINL
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Wang, S.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y., Yang, K.J., Yan, H.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B. Subrect Submission Submitted (17-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R. China
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Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., Ge Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Chther CSSs: CH230-313K4.TV
Chther CSSs: CH230-313K4.TV
Chther Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAP92648.1"
/db_xref="GI:33086672"
                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10116"
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Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plater: 313 row: K column: 4
class: BAC ends.
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Totoki,Y., Matanabe,H. and Sakaki,Y.
Totoki,Y., Matanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AG169335 654 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-037P16.T7, genomic survey
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Brain"
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/nore="Vector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
CHORI-230 Rat (BN/SsNHsd/MCW) BĀC library produced by
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BAC end sequences of Library RPCI-43
Unpublished
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100.0%; Pred. No. 9.3e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                'mol type="genomic DNA"
'strain="BN/SSNHsd/MCW"
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clone="CH230-313K4"
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1. .645
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Pan troglodytes
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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PRIMERS
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AG169335.1 GI:16699013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female
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606 GTTAATGGAGAGTGGCT 622
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BX169508/c
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BX169283/c
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Rat BAC End Sequences from Library CHORI-230 Mbol segment
Unpublished (1999)
Other_GSSS: CH230-246A22.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 302 Bmail: szhao@tigr.org
Clones are derived from the rat BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.digr.org/bacpac/or ering_information.html
Plate: 246 row: A column: 22
Class: BAC ends.
Locating AC action (1985)
Locating AC action (1985)
Locating AC action (1985)
Locating AC action (1985)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
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/TORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                   Gaps
                                                                                       /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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                                                                                                                                                                      85.0%; Score 17; DB 9; Length 654; 100.0%; Pred. No. 9.3e+02; Live 0; Mismatches 0; Indels
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/organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                             518 GTTAATGGAGAGTGGCT 502
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                                                                     /sex="male"
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                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 17; Conservative
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Entaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukaryota, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae; Danio.

Cypriniformes; Cyprinidae; Danio.

E 1 (bases 1 to 808)

S Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission-2003) The Sanger Institute, Wellcome Trust Genome Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hintcon, Cambridgeshire; CBIO 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Unpublished from the SP6 end of BAC 172C16. 172C16 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-JAN-2013) The Sanger Institute, Wellcome Trust Genome Submitted (27-JAN-2013) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

In humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 155N24.

Is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

| Keygene. Further details:
| Location/Qualifiers
         GSS 28-JAN-2003
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BX169283 10 128 bp DNA linear GSS 28-JAN-2
Danio rerio genomic clone DKEY-155N24, genomic survey sequence.
BX169283.1 GI:28000988
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Danio rerio genomic clone DKEY-172C16, genomic survey sequence.
EX169508
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 729)
Humphray,S.J., Huckle,E. and Durham,J.L.
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Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DK2":
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-172C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
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Danio rerio
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176 GCTGTTAATGGAGAGTGCCT 157
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CN210935.1 GI:46264785
                                             AW080408.1 GI:6035560
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Cardiff University
Museum Ave, BIOSI 2
Tel: +44 02920876703
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                                                                                                  sapiens (human)
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Matches 18; Conservative
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  seguence.
                                                                                                                              Homo sapiens
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SM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzae; Oryzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Organism="Oryza sativa (japonica cultivar-group)"
// Organism="Nipponbare"
// Cultivar-wipponbare"
// Clone="OSJNEf14H05"
// Clone="OSJNEf14H05"
// Clone="OSJNEf14H05"
// Clone="Noste="DH10B"
// Clone="DH10B"
// Clone="Nector: pBluescript II KS +; Site_1: EcoRI; Site_2: KhoI; Uninfected Control"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 31
4W080408/c
LOCUS
AW080408
DEFINITION xe53a08.x1 NCI_CGAP_Ut3 Home sapiens cDNA clone IMAGE:2611574 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                OSJNEI14H05.f OSJNEf Oryza safiva (japonica cultivar-group) cDNA clone OSJNEI14H05 5', mRNA sequence,
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                                                                                                  Length 808;
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larity 100.0%; Pred. No. 9.7e+02;
Conservative 0; Mismatches 0;
                                                                                                     Score 17; DB 9; Le
Pred. No. 9.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
/tissue_type="Testis"
/note="vector pindigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: H column: 05
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                        Mismatches
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Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                  812 bp
                                                                                                  Query Match
Best Local Similarity 100.0%; Pr
Matches 17; Conservative 0;
                                                                                                                                                                                                                                         247 CAGTTAATGGAGAGTGG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB684683.1 GI:29688408
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Matches 17; Conserv
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MACRESSION AND MAGE AND AND ADDRESS AND AD
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organism="Rattus norvegicus"
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Best Local Similarity 90.0
Matches 18; Conservative
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AUTHORS
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BE841809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Cadmium exposed rainbow trout subtractive"
/note="A subtractive cDNA library was produced to identify
genes that appear up-regulated in response to cadmium
toxicity. Technique was performed using the Clontech PCR
Select cDNA Subtraction Kit, using mRNA from control
(unpolluted) and cadmium exposed (65.7ug/L) 54-day old
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF410784 1inear EST 28-NOV-2000
UI-R-CNO-bml-a-02-0-UI.S1 UI-R-CNO Rattus norvegicus cDNA clone
UI-R-CNO-bml-a-02-0-UI 3', mRNA sequence.
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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized bladder library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 333)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 16.8; DB 7; Length 249; 90.0%; Pred. No. 1e+03; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                /organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/strain="Ugwey Seven-Spring"
/db_xref="taxon:8022"
/clone="Rt fcd_00G02"
/sex="FemaTe"
                                                      FUNDAMENT MIS
BACKWARD: MIS
Plate: 00 row: G column: 02
Seq primer: MIS-4
High quality sequence start: 16
High quality sequence stop: 237.
Location/Qualifers
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Genome Res. 6 (9), 791-806 (1996)
97044477
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Seg primer: M13 Forward
POLYA=Yes.
  Email: HurlerAL@cf.ac.uk
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rainbow trout.
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Best Local Similarity 90.07
These 18; Conservative
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                                             FORWARD: M13
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BF410784/c
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source

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/db xref="taxon:0116" / dev_zerge="taxon:0116" / dev_zerge="taxon:0116" / dev_zerge="taxon:0116" / dev_zerge="taxon:0116" / dev_zerge="taxon:0116" / dev_zerge="tayour" / dev_zerge='tayour" / dev_zerg='tayour" / dev_zerg='tayour' / dev_zerg='tayo
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1 (Dases I to 339)

1 (Dases I to 330)

2 (Dases I, Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F.F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pax: +55-11-2707001
Bmail: asimpsom@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR1-SN0065-220
500-006-d05&t3=2000-05-22&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 62
High quality sequence start: 62
High quality sequence stop: 338.
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MRI-SN0065-220500-006-d05 SN0065 Homo sapiens cDNA, mRNA sequence.
BE841809
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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mol_type="mRNA"
strain="Sprague-Dawley"
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/organism="Homo sapiens"
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/dev_stage="Adult"
/clone_lib="Ex0079"
/note="forgan: lung_normal; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
Gerived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 361)

1 (bases 1 to 361)

Dias No., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
Fax: +55-11-2707001
Fax: +55-11-2707001
This issimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0079-111100-474-e12&t5=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 343.
                                                                                                                                                       BF849242
CM3-EN0079-111100-474-e12 EN0079 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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1 GCAGTTAATGGAGAGTGGCT 20
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Homo sapiens
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BF521948
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BF849242
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                                                                                                /note=_organ: stomach normal, Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-Tibrary was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Endwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=463 Contact: Inge Arlart
KZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
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Rat ArrayTAG cDNA
Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Emall: www.rzpd.de
Emall: www.rzpd.de
Exzpp: LIOND463H12407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAAACAGCTATGAC.
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LIOND463H12407 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 2; Length 339; larity 90.0%; Pred. No. 1.1e+03; Conservative 0; Mismatches 2; Indels
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                        /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
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        'mol_type="mRNA"
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REFERENCE AUTHORS

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE PUBMED COMMENT JOURNAL

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Produrement: Jeff Struewing, M.D., Michael R. Emmert-Buck,
Tissue Produrement: Jeff Struewing, M.D., Michael R. Emmert-Buck,
Tissue Produrement: Jeff Struewing, M.D., Michael R. Emmert-Buck,
Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA
Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Insert Length: G.E. Consortium/LLNL at:
Insert Length: 57 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 372.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue type="normal epithelium"
/lab host="DH10B"
/clone lib="NCT CGAP Ov38"
/note="Organ: Ovary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
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1 (Dases 1 to 379)
Hillier,L.; Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulran,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohling,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,F. and
                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                 1 (bases 1 to 374)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%; Score 16.8; DB 1; Length 374; 90.0%; Pred. No. 1.1e+03; ive 0; Mismatches 2; Indels C
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2549831"
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                                                                 AI954046.1 GI:5746356
                                                                                                                                  Homo sapiens (human)
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mRNA sequence.
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//organism="kattus norvegicus"
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//do_trafe="mkna"
//do_trafe="wkna:1016"
//dov_stage="adult"
//dov_dov="adult"
//dov="adult"
//dov="adult
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bento-soares@uiowa.edu

CDNA Libbary Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.B. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1791356

Seq primer: M13 Forward.
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Rattus norvegicus
Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 319 335 8250
Fax: 319 335 9565
Email: L---
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84.0%; Score 16.8; DB 2; Length 372;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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BF521948.1 GI:11629915
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                                                                                                                                                                                                                                                                                                                                                     discovery
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8889548
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source

FEATURES

A1954046/c LOCUS DEFINITION

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Gaps 0

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BF542969 11-DEC-2000 UL-R-YO-abi-e-06-0-UI.rl UL-R-YO Rattus norvegicus cDNA clone UL-R-YO-abi-e-06-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Scares, MB
Contacts Scares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
584: 319 335 9556
Email: bento-scares@uiowa.edu
Email: bento-scares@uiowa.edu
Email: bento-scares@uiowa.edu
Email: bento-scares@uiowa.edu
CDNA Library Preparation: M.B. Scares Lab Clone distribution:
Clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LiML (Info@ninge.llnl.gov): IMAGE ID= 1790988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo.
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Rattus norvegicus
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IVAGE:323151"
/tissue_type="senescent fibroblast"
/lab host="#1010B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts_NbHSF"
/note="weeter: pt773D (Pharmacia) with a modified
polylinker V TYPE: phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 390)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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/strala="Sprague-Dawley"
/bxref="texon:10116"
/clone="UI-R-Y0-abi-e-06-0-UI"
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97044477
8889548
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/organism="Homo sapiens"
Seq primer: MoD.kach.c. 333.
High quality sequence stop: 333.
Location/Qualifiers
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Best Local Similarity 90.0
Matches 18; Conservative
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TITLE
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BF542969
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//dev_grage="5 year old"
/lab_hoet="DH10B (amplication in resistant)"
/lab_hoet="DH10B (amplication in the state of the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W42610 are senescent_fibroblasts_NbHSF Homo sapiens CDNA clone_IMAGE:323151 5', mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 379)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                    Insert Size: 3093
High quality sequence stops: 348
Source: IMAGE Consortium, LLNL, frontact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 3093 Std Brror: 0.00
Seq primer: Promega -21ml3
High quality sequence stop: 348.
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Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
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84.0%; Score 16.8; DB 7; Length 379;

Best Local Similarity 90.0%; Pred. No. 1.18+03;

Matches 18; Conservative 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRXN%"
/db_xref="GDB:3846877"
/db_xref="taxon:9606"
/clone="IMAGE:190468"
       Email: est@watson.wustl.edu
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W42610.1 GI:1327090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="male"
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W42610
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ORIGIN

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Homo sapiens (human)
Homo sapiens
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d
/dev_stage="adult"
/lab_host="DH108 (Life Technologies)"
/clone_lib="UL-R-Y0"
/clone_lib="UL-R-Y0"
/note="Vector: p773D-pac (Pharmacia) with a modified
/note="Vector: p773D-pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco_RI; The UI-R-Y0
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-A) UI-R-E0,
UI-R-E1, UI-R-C0, and UI-R-C1). The tag is a string of
J-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library of ones from
which 3' ESTS had been derived whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
library. This procedure has been previously described
library. This procedure has been previously described
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(Dases 1 to 393)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: m13 -40 forward
High quality sequence stop: 261.
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yy42f09.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:273929 3', mRNA sequence,
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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84.0%; Score 16.8; DB 2; Length 390;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels C
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/db_xref="GDB:3883571"
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N33486/c
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capaba-rement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Eissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDM Library Preparation: Life Technologies, Inc.
CDM Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.thum/
Insert Length: 2770 Std Error: 0.00
Stg primer: -40UP from Gibco
High quality sequence stop: 4106
POLYA-No.
                                                                ALSSYJZZ TIG-WAR Tinear EST 13-WAY-1999
tq41f08.x1 NCI_CGAP_Ut1 Homo sapiens CDNA clone IWAGE:2211591 3',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases 1 to 410)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index.
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:2211591"
db_xref="taxon:9606"
|clone="IMAGE:273929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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186

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REFERENCE AUTHORS

DEFINITION

RESULT 44 W42606/c

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1 (Dases 1 to 415)

1 (Dases 1 to 415)

1 (Dases Phttp://www.ncbi.nlm.nih.gov/ncicgap.

1 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

1 Tumor Gene Index

1 (Dubblished (1997)

1 Contact: Robert Strausberg, Ph.D.

1 Email: Cgapbs-rémail.nih.gov

1 NOTE - This CGAP library is from RAT Tissue Procurement: Dr.

1 Maarten Bosland, NYU

1 CDNA Library Preparation: Life Technologies, Inc.

2 CDNA Library Preparation: NGI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:

1 Info@nimage: Library Angleson Gibco

2 Seq primare: -40UP from Gibco

3 High quality sequence stop: 388.
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yg89c07.81 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:40831 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:10116"
/db xref="taxon:10116"
/clone="twdE:3122103"
/lab_host="DH10B (phage-resistant)"
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/clone lib="NLI CGAP_PR35"
/note="Corgan: prostate; Vector: pCMV-SPORT6; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: 01 go dr. Average insert size 2 kb. Library constructed by Life Technologies.
         BE349791 415 bp mRNA linear EST 18-JUL-2000 hq43b08.xl NCI CGAP_Fr35 Rattus norvegicus cDNA clone IMAGE:3122103 3', mRNA sequence.
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(Dases 1 to 417)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,M., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                       Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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84.0%; Score 16.8; DB 2; Length 415;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
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/organism="Rattus norvegicus"
                                                                                                                                                                                       Rattus norvegicus (Norway rat)
Rattus norvegicus
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The WashU-Merck EST Project
Unpublished (1995)
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/strain="WU/HSD"
                                                                                                                              BE349791.1 GI:9261644
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Homo sapiens
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R55760.1 GI:825835
EST.
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R55760/c
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/mol_type="mixmo" supress
/db_xref="dbB:1254663"
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/dlone="type="senescent fibroblast"
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/tlab_host="pilub (ampidillin resistant)"
/clone_lib="Soares senescent fibroblasts NbHSF"
/clone_ib="Soares senescent fibroblasts NbHSF"
/clone="vector: pirf3D (Pharmācia) with a modified
polylinker V TYPE: phagemid; Site_1: Not I; Site_2: Eco
polylinker trand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                                                                                                                                                                                           W42606 2C23d08.s1 Soares senescent_fibroblasts_NbHSF Homo sapiens CDNA_clone_IMAGE:323151_3', mRNA_sequence.
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Whison, R.

Unpublished (1995)
Contact: Wilson RK.
Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 1600 Fax: Movellable royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.MSGA+ET
High quality sequence stop: 391.
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(bases 1 to 413)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
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                        Query Match

84.0%; Score 16.8; DB 1; Length 410;

Best Local Similarity 90.0%; Pred. No. 1.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels (
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/organism="Homo sapiens"
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W42606.1 GI:1327036
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Best Local Similarity
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Wilson, R

TITLE JOURNAL COMMENT

PEATURES

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Gaps

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Populus tremula x Populus tremuloides

SM Populus tremula x Populus tremuloides

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosida I; Malpighiales; Salicaceae; Saliceae; Populus.

E (bases 1 to 431)

Sterky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P.,

Brunner, A.M., Campaa, L., Jonsson-Lindvall, J., Tandre, K.,

Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P.,

Nilsson, O., Sandberg, G., Karlsson, J., Lundeberg, J. and Jansson, S.

A Populus EST resource for functional genomics

Unpublished (2003)

Cottact: Bo Segerman

Umea Plant Science Center, Department of Plant Physiology
      /mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK100560 431 bp mRNA linear EST 01-DEC-2003 C050P42.5pR Populus strain T89 leaves Populus tremula x Populus tremuloides cDNA clone C050P42 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA350346 Locain Homo sapiens CDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid F5789.2, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/strain="T89"
                                                                                                                                                                                                                                                    Length 418;
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/clone==c050842"
/tissue type="leaf"
/clone_lib="Populus strain T89 leaves"
                                                                                                                                                                                                                                                  84.0%; Score 16.8; DB 7; 90.0%; Pred. No. 1.1e+03; iive 0; Mismatches 2;
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Location/Qualifiers
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Tel: +46 90 786 5279
Fax: +46 90 786 6676
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 18; Conservative
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AA350346
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DEFINITION
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CK100560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: escewatson.wustl.edu
Insert Size: 1665
High quality sequence stops: 349 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1665 Std Error: 0.00
Seq primer: Promega -21m13
High quality sequence stop: 349.
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Regenerative Medicine
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 418)

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230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 418 Std Error: 0.00.
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E 1 (bases Luc 440)

E Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., White, Y., Wylle, T., Reptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Restston, R. and Wilson, R. Theising, B., Washb-Merck EST Project 1997

L Unpublished (1997)

Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               440 bp mRNA linear EST 30-MAY-1997 2v24g02.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:754610 AA436245. AA436245.1 GI:2141159 EST.
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                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.

1 (Dases 1 to 432)

Adams, M.D., Kerlavage, A.R., Fields, C. and Venter, J.C.

3,400 expressed sequence tags identify diversity of transcripts from human brain

Nat. Genet. 4, 256-267 (1993)
                                                                                                                                                                                                                                                                                                                                                                                 The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
9713 Medical Center Drive, Rockville, MD 20850 USA
9713 Medical Center Drive, Rockville, MD 20850 USA
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
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/note="Organ: brain; Vector: lafmid_BA; Site_1: HindIII;
Site_2: NotI"
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/esk="female"
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                                                                                                                                                                                                                                                                                                                    Other ESTS: EST57668 THC192694
Contact: Kerlavage, AR
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This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41ml3 fwd. Er from Amersham High quality sequence stop: 367.
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Matches 18; Conservative 0; Mismatches 2; Indels
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/organism="Homo sapiens"
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                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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   | .4 72.0 12766 4   | .4 72.0 12817 6                                      | .4 72.0 12949 3  | .4 72.0 13182 10  | .4 72.0 13269 6  | .4 72.0 13274 6    | .4 72.0 13829 11  
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|   | . 17.0 17.0 2 AMERICAN AMERICA | 1.4 72.0 1176 6 ARGATT80 ARGATT80 Listeria C 899 14.2 71.0 203 1 ARGATT80 A | Hand State                               | Hand State         | Additional | Additional | ACADESTS AND ACADESTS AND ACADESTS AND ACADESTS | Main Properties   Main Prope | Additional Approximation Appro | Additional | ACADEMIC ADDRESS ACADEMIC C B99 14.2 71.0 203 1 ADDRESS ACADEMIC C B99 14.2 71.0 203 1 ADDRESS ACADEMIC C B99 14.2 71.0 203 1 ACDS 719 ACADEMIC C B99 14.2 71.0 211 10 ACDS 719 ACADEMIC C B90 14.2 71.0 241 B ACADEMIC C B90 14.2 71.0 261 A AAI 29384 | Acal Section 17.0 17.0 17.0 203 12 Anniolist Acal Section 17.0 203 12 Anniolist Acal Section 17.0 203 12 Anniolist Acal Section 17.0 21.0 10 Anniolist Acal Section 17.0 21.0 21.0 Anniolist Acal Section 17.0 22.0 14.2 71.0 24.1 B ACAN 2465  4 72.0 2235 10 ADB69874 Anniolist Acal Section 17.0 26.1 B | Acception Application of Acception A | Abd67780 Listerial C 899 14.2 71.0 203 12 AbN40517 Aca18661 Prokaryot 901 14.2 71.0 241 0 AbC92231 Aca2858 Prokaryot 902 14.2 71.0 241 0 AbC92231 Aca2858 Aca47696 Arabidops 903 14.2 71.0 241 0 AbC92231 AdC62250 Transcrip 904 14.2 71.0 241 0 AbC92231 Adc62250 Transcrip 904 14.2 71.0 241 0 AbC92231 Adc62250 Transcrip 904 14.2 71.0 241 0 Ab146507 Adb69874 C necfor 906 14.2 71.0 241 0 Ab120357 Adb69874 Adb69874 C necfor 907 14.2 71.0 241 AA129357 Adb69874 Adb69875 Adb69875 Adb69876 Adb69876 Adb69877 Adc72306 Adb69877 Adc72306 Adb69877 Adc72306 Adb69877 Adc72306 Adb69877 Adc72306 Adb69877 Adc72306 Adb69877 Adc7230 Ad | Application Applic | Maintain            | Accordance   Accodd   Accordance   Accordance   Accordance   Accordance   Accordance   Accordance   Accordance   Accordance   Accordance   Accorda | Accession           | Mage 7781   Mage 7782   Mage | ## 72.0   1176 6 ARGENTON ADDRESSES PROKARYOL   900   14.2   71.0   203   12 ARM10517   ## 72.0   1176 6 ARGENTON ADDRESSES PROKARYOL   900   14.2   71.0   234   10 ARD55719   ## 72.0   1156 3 AAG47656 | Maintain            | 1176   ARG67180   ARG67180   Liseria   C   899   14.2   71.0   203   12   ARG6718   ARG67180   Liseria   C   899   14.2   71.0   203   12   ARG6718   ARG71864   ARG71864   ARG71864   ARG71866   ARG71868   ARG71868   ARG71868   ARG71868   ARG71868   ARG71868   ARG71868   ARG71868   ARG71868   ARG71869   ARG71868   ARG71869   AR | Accordance   Acc | 17.0   1176   ABG/730   AAG/186   ACALBEAN   AAG/186   ACALBEAN   AAG/186   ACALBEAN   AAG/186   ACALBEAN   AAG/186   ACALBEAN   AAG/186   ACALBEAN   AAG/186   AAG/ | 116   ARG67780   ARG67780   ARG6780   ARG678 | 17.0   17.0 | 17.0   1177   6 ARBGOTROL   ARBGOTROL | 17.0   17.0   A. | 117.0   ADMINISTRATION   ADMINISTRATIO | 117.0   6.000   1.0 | Accordance   Acc | 117.6   6 MBG/6790 | 1176   6 Mag(5790)   Amag(7790)   Amag(779 | 72.0   1176   6 ACADSSSS | The control of the | 1175   1176   120   12 | 1175   1176   1200 | A. CALLEGE   ACAZISES   PROMERYOR   STATE   STATE | The control of the | 11.16   F. A.C. A.C. A.C. A.C. A.C. A.C. A.C. A | 7.2.   11.76   A. CALDEGO   A | 7.20   11/16   E. ACATASSES   PROCRATOR   C. ACATASSES   C | 11.00   6 ARANGES   ACADES   ACADES | 11.00   6 ARANGES   ARAN | The control of the | Maintaine   Main | The Control of Medicard   Medic | The control of the | The control of the | The control of the | The control of the | The control of the | The control of the | The control of the | 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, | 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, | 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, | 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, | 1177   1177   170   17 | 10   10   10   10   10   10   10   10 | Marches   Marc | The control of the | 1177       | 11   11   12   12   13   13   14   15   15   15   15   15   15   15 |

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ABN84786 

Homo sapiens

24-JUL-2002.

(RUBI/) RUBIN B Y. (ANDE/) ANDERSON S L.

condition 88888888888888888888888888888888888 Abl19047 Droscophil Ac120628 DNA clone Abk53382 Human eos Abv6667 Human pro Ac120630 DNA clone Ac120630 DNA clone Ac120643 DNA clone Ac120643 DNA clone Ac120645 DNA clone Ac120649 DNA clone Ac120649 DNA clone Ac120659 DNA clone Ac120650 DNA clone Ac120651 DNA clone Ac120652 DNA clone ABV06667 ACL20630 ACL20627 ACH74720 ACL20654 ACL20657 ABK78758 ADC76060 ABV36615 

ALIGNMENTS

ABN84786 standard; DNA; 20 BP 05-NOV-2002 (first entry) ABN84786;

Primer useful for familial dysautonomia allele genotype analysis. diagnosis; SSCP;

Familial dysautonomia; Riley-Day syndrome; hereditary sensory neuropathy III; human; carrier; lkappaB kinase-complex associated protein; primer; single-strand conformational polymorphism; ss.

EP1225232-A2.

17-JAN-2002; 2002EP-00001232.

17-JAN-2001; 2001US-0262284P.

Rubin BY, Anderson SL

WPI; 2002-601228/65.

Detecting a polymorphism in a gene encoding the lkappaB kinase-complex-associated protein is used to diagnose and identify carriers of familial dysautonomia.

Claim 7; Page 9; 16pp; English

The invention provides a method for detecting a polymorphism linked to a disruptive mutation in a gene encoding the ItappaB kinase-complex.

a disruptive mutation in a gene encoding the ItappaB kinase-complex.

a sociated protein (IKAP) on chromosomes with the major FD haplotype, a IKAP-encoding gene showed, in chromosomes with the major FD haplotype, a IKAP-encoding gene showed, in chromosomes with the major FD haplotype, a CT to C transition in position of of the donor splice site of intron 20.

This mutation (2507+6T to C) results in the generation of an IKAP mRNA in which exon 20 is spliced out along with intron 20. Sequence analysis of the IKAP gene of individuals heterozygous for the Profession of most common minor haplotype (minor 2) showed a G to C transversion of not encounted in a property and property of the reported IKAP CNNA, resulting in an a Argósspro aminor able substitution and disruption of a consensus Ser/hhr kinase phosphorylation site. The present sequence is a primer that can be used in a claimed method for detecting a disruptive mutation in the IKAP gene, using single-strand conformational polymorphism (SSCP) analysis.

The primer was used in the genotype analysis of FD alleles. Use with the probands homozygous for the major and minor 2 FD reports were homozygous for the major haplotype, all affected individuals were homozygous for the major and minor 2 FD cother parent and the proband were heterozygous for the major and minor 2 FD cother parent and the proband were heterozygous for the major for the probands were homozygous for the major FD haplotype and minor 2 FD cother parent and the proband were heterozygous for the major for the probands were common for the major for the probands were common for the major for the probands were homozygous for the major for the probands were homozygous for the major for the probands were homozygous for this mutation, and 4 siblings of the probands were homozygous for the major and the 2507+6T to C mutation of the presence of 25 carriers of 2507+6T to ö Gaps ö Query Match
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other; 1 GCAGTTAATGGAGAGTGGCT 20 20 GCAGTTAATGGAGAGTGGCT 임

ABQ80567 standard; DNA; 66479 ABQ80567; RESULT 2

ВР

08-NOV-2002 (first entry) 

Mutant human IKBKAP gene #2.

Human; IXBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening; FD2; mutation; gene; chromosome 9q31; ds.

Homo sapiens.

Synthetic.

Location/Qualifiers replace(33714,G) mutation

WO200259381-A2

01-AUG-2002.

07-JAN-2002; 2002WO-US000473.

06-JAN-2001; 2001US-0260080P.

(GEHO ) GEN HOSPITAL CORP.

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Slaugenhaupt S,
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                                                                                                                                                         The present invention relates to methods and compositions useful for detecting mutations which cause Familial Dysautonomia (FD, Riley-Day syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OWIM) Syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) (OWIM) Care associated with FD. The mutations in the NERAP gene (see AB080565) are associated with FD. The mutation associated with the major haplotype of FD. FDI mutation, is a base pair (bp) mutation, where the thymine of FD. FDI mutation, is a base pair (bp) mutation, where the thymine of FD. The results in skipping of exon 20 in the mRNA from FD patients, although they continue to express varying levels of wild-type message in a tissue-specific manner. The mutation associated with the minor haplotype, FD2 mutation, is a bp mutation where the guanine nucleotide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine. This by mutation causes an arginine to proline missense mutation (R696P) in the IKBKAP protein, which is predicted to disrupt a potential phosphorylation site. The IKBKAP nucleic acid sequences are useful for identifying a subject with FD and for rapid carrier screening. The IKBKAP sequence was not shown in the specification, but was derived from the human wild-type IKBKAP sequence given in Fig 6 human wild-type IKBKAP sequence given in Fig 6
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                                                     New IKBKAP genes with mutations, useful for identifying a subject with familial dysautonomia (FD), or for rapid carrier screening in the Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or prenatal diagnosis.
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Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
FDI; mutation; gene; chromosome 9q31; ds.
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   Slaugenhaupt S, Gusella JF;
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The present invention relates to methods and compositions useful for detecting mutations which cause Familial Dysautonomia (FD, Riley-Day syndrome, Heredditary Sensory and Autonomic Neuropathy Type III) [OMIN 223900]. It was found that mutations in the IKBKAP gene (see ABQ80565) are associated with FD. The mutation associated with the major haplotype of FD mutation, here the thymine of FD FD mutation, where the thymine cof FD; FD mutation, where the thymine of intron of intron of oin the IKBKAP gene is replaced with a cytosine. This results in skipping of exon 20 in the mRNA from FD patients, although they continue to express varying levels of wild-type corresponds in a lissue-specific manner. The mutation, where the quanthe minor haplotype, FD2 mutation, is a bp mutation, where the guanthe conclectide at bp 2397 (bp 73 of exon 19) is replaced with a cytosine. This bp mutation associated with a cytosine. This bp mutation associated with a cytosine. The IKBKAP protein, which is predicted to disrupt a potential consumes an aubject with FD and for rapid carrier screening. The IKBKAP contains 37 exons and maps to chromosome 9931. Note: the present sequence was not shown in the specification, but was derived from the thuman wild-type IKBKAP sequence given in F19 6
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                                                                                       New IXBKAP genes with mutations, useful for identifying a subject with familial dysautonomia (FD), or for rapid carrier screening in the Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or prenatal diagnosis.
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Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
FDI; FD2; mutation; gene; chromosome 9g31; ds.
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replace(34201,T)
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Gusella JF;
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(GEHO ) GEN HOSPITAL CORP.

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                                                      Claim 1; Page; 109pp; English.
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          Slaugenhaupt S, Gusella JF
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                                                                                                                                                                                                                                                                                                                                                       The present invention relates to methods and compositions useful for detecting mutations which cause Familial Dysautonomia (FD, Riley-Day syndholds) and Autonomic Neuropathy Type III) [OMIM Syndhold II was found that mutations in the NEERAP gene (see ABQ80565) are associated with FD. The mutation is absenged with the major haplotype of FD. FDI mutation, is a base pair (bp) mutation, where the thymine nucleotide located at bp 6 of intron 20 in the IKBKAP gene is replaced with a cytosine. This results in skipping of exon 20 in the mRNA from FD patients, although they continue to express varying levels of wild-type message in a tissue-specific manner. The mutation associated with the minor haplotype, FD2 mutation, is a bp mutation associated with a cytosine. This bp mutation causes an arginine to proline missense mutation (R696P) in the IKBKAP process, which is predicted to disrupt a potential phosphorylation site. The IKBKAP nucleic acid sequences are useful for identifying a subject with FD and for rapid carrier screening. The IKBKAP gene contains 37 exons and maps to chromosome 9931. Note: the present sequence, was not shown in the specification, but was derived from the
                                                                                                                                           New IKBKAP genes with mutations, useful for identifying a subject with familial dysautonomia (FD), or for rapid carrier screening in the Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or prenatal diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66479 BP; 18271 A; 12400 C; 14128 G; 21680 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human wild-type IKBKAP sequence given in Fig 6
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ö Gaps ö 100.0%; Score 20; DB 6; Length 66479; 100.0%; Pred. No. 6.9; 0; Indels 0; Mismatches

33581 GCAGTTAATGGAGAGTGGCT 33600

Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome; Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening; gene; chromosome 9931; ds.

The present invention relates to methods and compositions useful for detecting mutations which cause Familial Dysautonomia (PD, Riley-Day Syndrome, Hereditary Sensory and Autonomic Neuropathy Type III) [OMIM 233900]. It was found that mutations in the IKBAAP gene (the present sequence) are associated with FD. The mutation associated with the major haplotype of FD, FDI mutation, is a base pair (bp) mutation, where the thymine nucleotide located at bp 6 of intron 20 in the IKBAAP gene is replaced with a cytosine. This results in skipping of exon 20 in the mRNA from FD patients, although they continue to express varying levels of wild-type message in a tissue-specific manner. The mutation associated with the minor haplotype, FDZ mutation, is a bp mutation, where the cytosine. This bp mutation causes an arginine to proline missense mutation (R696P) in the IKBKAP protein, which is predicted to disrupt a potential phosphorylation site. The IKBKAP undled capid carrier screening. The IKBKAP gene contains 37 exons and maps to chromosome 9431 ; New IKBKAP genes with mutations, useful for identifying a subject with familial dysautonomia (FD), or for rapid carrier screening in the Ashkenazi Jewish population, e.g. screening presymptomatic homozygotes or prenatal diagnosis. Gaps Sequence 66479 BP; 18271 A; 12398 C; 14129 G; 21681 T; 0 U; 0 Other; ö 6; Length 66479; 0; Indels Score 20; DB 6 Pred. No. 6.9; 0; Mismatches 33581 GCAGTTAATGGAGAGTGGCT 33600 1 GCAGTTAATGGAGAGTGGCT 20 . 0 Claim 1; Fig 6; 109pp; English. 100.08; Query Match Best Local Similarity 100.0%; Matches 20; Conservative (

AAK69857 standard; DNA; 22791 BP.

(first entry)

06-NOV-2001

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24669.

Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.

Homo sapiens

WO200157182-A2.

09-AUG-2001

2000US-0186350P. 2000US-0189874P. 2000US-0190076P. 2000US-0198123P. 2000US-0205515P. 2000US-0180628P. 2000US-0184664P. 17-JAN-2001; 2001WO-US001354. 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-AFR-2000; 19-MAY-2000; 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 

2000US-0216880P. 2000US-0217487P. 2000US-0217487P 2000US-0217496P 28-JUN-2000;

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14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225214P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-022526FP.
14-AUG-2000; 2000US-022575FP.
14-AUG-2000; 2000US-022576FP.
14-AUG-2000; 2000US-0231414P.
08-SEP-2000; 2000US-0231414P.
08-SEP
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08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249214P.
17-NOV
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c acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis. Nucleic auseful fo

Disclosure; SEQ ID NO 24669; 3071pp + Sequence Listing; English.

AAMS1951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or complement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially

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Gaps

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The invention relates to an isolated polynuclectide (I) comprising: (a) any of a group of over 4000 nuclectide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences that hybridize to (a), under moderately to (a); or (f) degenerate variants of (a). Polypeptides (ABP6856-ABF68637) encoded by (I) and oligonuclectide can be used to detect cancer in a patient and compositions comprising polypeptides, polynuclectides, antibodies, fusion proteins, T cell populations and antigon presenting cells expressing the polypeptide are useful in treating pancreatic cancer probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene
                           to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention
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cancers and cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
cytostatic; tumour; gene; ss.
                                                                                                                                                                Sequence 22791 BP; 5528 A; 5289 C; 5688 G; 6286 T; 0 U; 0 Other;
                                                                                                                                                                                                                               87.0%; Score 17.4; DB 4; Length 22791; 94.7%; Pred. No. 1.3e+02; ative 0; Mismatches 1; Indels 0;
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2001US-0287112P.
2001US-0291631P.
2001US-0305484P.
2001US-0313999P.
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2001US-0265682P.
2001US-0267568P.
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tes 18; Conserv
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20-AUG-2001;
27-NOV-2001;
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28-APR-2001;
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09-FEB-2001;
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                                                                                                                                                                                                                                  Query Match
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ABV98005/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing full length cDNA clones and their use
therapy. Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly
                                                                                                                                              Gaps
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T, Koga H;
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                                                                                                      ch 84.0%; Score 16.8; DB 6; Length 589; 1. Similarity 90.0%; Pred. No. 1.5e+02; 18; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 3314; 1380pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
                                                                     Sequence 589 BP; 189 A; 117 C; 110 G; 172 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nishikawa T, Isogai T, Hayashi K, Ishii S, su A, Sugiyama T, Nagai K, Kojima S, Otsuki
                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                  Human full-length cDNA, SEQ ID NO: 3314.
                                                                                                                                                                                                                 123 GCTGTTAATGGAGAGTGCCT 104
                                                                                                                                                                                 1 GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                                                                                            AAK94484 standard; cDNA; 2637 BP.
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Best Local Similarity 90...
Best Local Similarity 90...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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This invention describes novel nucleic acid (cDNA) sequences (A) which have anticancer activity and are highly expressed in ovarian tumor tissue (and some also in testis and breast cancer tissue). The products of the invention can be used for gene therapy. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of ovarian cancer; (ii) directly for treating this form of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTS from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a tissue. Associated with the human obtain tumor CDNA library derived EST fragments represented in AAY76505-Y76638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences expressed in ovarian, and some other, cancer tissues, and derived polypeptides, for treatment of ovarian cancer and identification of therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
Expressed sequence tag; EST; human; ovarian tumor; anticancer; gene therapy; treatment; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 16.8; DB 2; Length 2878; 90.0%; Pred. No. 1.9e+02; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                     Hinzmann B, Schmitt A, Pilarsky C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2878 BP; 776 A; 680 C; 628 G; 794 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 193; 310pp; German.
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Best Local Similarity 90.0<sup>1</sup>
Matches 18; Conservative
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                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA from clone of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
                                                                                                                                                                                                                                                                                                                                                human; medicine; signal transduction; glycoprotein; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Best Local Similarity 90.0%; Pred. No. 1.98+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2637 BP; 716 A; 626 C; 586 G; 709 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian tumor cDNA library derived EST fragment 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 3314; 1340pp; English
                                                                                                                                                                                                                                                                                               Full length human cDNA clone SeqID 3314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 GCAGTCAATGGAGAATGGCT 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCAGTTAATGGAGAGTGGCT 20
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                  873 GCAGTCAATGGAGAATGGCT 892
                                                                                                                                          ADL31281 standard; cDNA; 2637 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                             oligo-capping method; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99JP-00194486.
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P-PSDB; ADL31282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP1396543-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-APR-2000
                                                                                                                                                                                                                                           20-MAY-2004
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                                                                                                                                                                                             ADL31281;
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AAZ77516
ID AAZ77
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AC AAZ77
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DT 10-AP
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                                                                                         RESULT 9
ADL 1281
ADL 1281
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ADL 1281
ADL 20-
DIT 20-

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Gaps

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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for spressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amin acid sequences. AASS4197-AASS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences. ÅAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 19697; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                   Tang YT;
  30-MAR-2001; 2001WO-US008631
                                             31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                                                                                                                                                                              WPI; 2001-639362/73.
P-PSDB; ABG19706.
                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                             biodiversity.
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Gaps ô 84.0%; Score 16.8; DB 5; Length 4071; 90.0%; Pred. No. 2e+02; Live 0; Mismatches 2; Indels 0. Sequence 4071 BP; 1115 A; 935 C; 935 G; 1086 T; 0 U; 0 Other; Local Similarity 90.0 nes 18; Conservative Query Match Best Loc Matches

ABL61892 standard; DNA; 4977 BP 15-MAY-2002 (first entry) ABL61892; RESULT 12 ABL61892
ID ABL6
XX AC.
XX XX
XX XX
XX XX
XX XX
XX XX
XX XX
XX YCOT
XX

Colon adenocarcinoma related gene sequence SEQ ID NO:229.

Human, cancer; colon, breast, ovary; oesophagus, kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma; gene; ds.

Homo sapiens

WO200194629-A2

13-DEC-2001

2000US-0235711P. 2000US-0235720P. 2000US-0235840P. 2000US-0235863P. 2000US-0235028P. 2000US-0236032P. 2000US-0236033P. 2000US-0236034P. 2000US-0236109P. 30-MAY-2001; 2001WO-US010838. 2000US-0234034P. 2000US-0234052P. 2000US-0234509P. 2000US-0234567P. 2000US-0234924P. 2000US-0233133P 2000US-0233617P 2000US-0234009P 2000US-0235638P. 2000US-0235082P 2000US-0245084P 20-SEP-2000; 2 20-SEP-2000; 2 20-SEP-2000; 2 22-SEP-2000; 2 22-SEP-2000; 2 25-SEP-2000; 2 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 25-SEP-2000; 26-SEP-2000; 28-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000; 28-SEP-2000; 01-NOV-2000; 27-SEP-2000; 28-SEP-2000 28-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 03-OCT-2000; 28-SEP-2000 03-OCT-2000 03-OCT-2000, 03-OCT-2000 02-OCT-200

(AVAL-) AVALON PHARM.

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Horrigan S; Endress G, Carter KC, Ebner R, Augustus M, Weaver Z; Young PE, Soppet DR,

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 229; 44pp; English.

The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in Abl61664 to Abr70110), or is at least S\$ identical to (S), where a change in corpression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such properties of the agent. M1 can be used in the treatment of cancer such properties of the agent, M1 can be used in the treatment of cancer such prostate or pancreatic cancer, adenocarcinoma, clear cell cancer, infiltrating lobular cancer, squamous

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ADL83261;
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Wu TD;
                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL83261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of GS is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating (MS) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasals; rheumatoid arthritis; perilonephritis; asthma; thrombosis; cardiac repertusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; according sericodontal disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                           Seguence 4977 BP; 1394 A; 1147 C; 1042 G; 1394 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                         Human cDNA differentially expressed in granulocytic cells #800.
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                                                                    84.0%; Score 16.8; DB 6; Length 4977; 90.0%; Pred. No. 2e+02; ive 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                     granulocytic cell; DNA chip; bacterial infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vockley J;
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                                                                                                                                1 GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                    ABK84229 standard; cDNA; 4977 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2000; 2000US-0237189P.
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                    18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOGIC INC.
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                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                              14-AUG-2002
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                                                                                                                                                                                                                                                               ABK84229;
                    tumour
                                                                                                       Matches
                                                                                                                                                                                                                         ABK84229
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is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful

CC for screening an agent capable of modulating GA, M3 is useful

CC inflammation in a tissue, M4 is useful for detecting an inflammation

CC inflammation in a tissue, M4 is useful for detecting an inflammation

CC specially chronic; in a tissue, an allergic response in a subject,

CC sporiasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,

CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult

CC disease, ulcerative colitis, periodontal disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial

CC disease, ulcerative colitis, periodontal disease; also bacterial

CC fungal infection and M5 is useful for treating one of the above

CC onditions. The present sequence represents a gene differentially

CC fungal infection wide: Note: The sequence data for this patent did

CC onditions. The present sequence represents a gene differentially

CC form part of the printed specification, but was obtained in

CC ftp.wipo.int/pub/published_pct_sequences

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.0%; Score 16.8; DB 6; Length 4977; 90.0%; Pred. No. 2e+02; cive 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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nes 18; Conservative
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P-PSDB; ADL83262.
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The present sequence is that of pig nor-1 nuclear receptor nucleic acid AJ011767. Nor-1 has been identified as a molecular target for therapeutic intervantion in the treatment of myeloid leukaemia. The invention provides methods of inhibiting the proliferation of a haematopoietic stem cell or a haematopoietic myeloid cell by modulating the level of a nor-1 and/or nur77 nuclear receptor. This involves increasing the level of the receptor polypeptide or polynucleotide, e.g. by administration of a vector comprising the polynucleotide. A claimed method of treating leukaemia comprises modulating a nor-1 and/or nur77 nuclear receptor in a haematopoietic stem cell or myeloid cell. Also claimed are methods of identifying an upregulator of expression of nor-1 and/or nur77, of identifying a compound for the treatment of leukaemia, and of screening for a compound for the treatment of leukaemia, and of screening
hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's lymphoma, intermediate lymphoma, follicular lymphoma, type II hyppersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, mysathemia gravis, hypoadcenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting proliferation of a hematopoietic cell, useful for treating or preventing leukemia, comprises modulating the level or activity of nor-1 and/or nur?? nuclear receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig; nor-1; nuclear receptor; receptor; leukaemia; gene therapy; cytostatic; haematopoietic cell; ds.
                                                                                                                                                                                                                                                          Sequence 4977 BP; 1394 A; 1147 C; 1042 G; 1394 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  84.0%; Score 16.8; DB 12; Length 4977; 90.0%; Pred. No. 2e+02; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pig nor-1 nuclear receptor nucleic acid AJ011767.
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                                                                                                                                                                                                                                                                                                                                                                                        1 GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF28873 standard; DNA; 5115 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-2003; 2003WO-US011804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 18; Conserv
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Milbrandt J;

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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX aequences have activities such as: cytostatic; hepatotropic; vulnerary; antiposoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory, antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarkinsonian; nootropic; neuroprotective; immunostimulant; thrombolytic; antiarkinsonic; antidiabetic; hypotensive, fermatological; immunosuppressive; antidiafammatory; antiarasmic; gene therapy; cancer; proliferative disorder; antibarcerial; antifungal; antitheumatic; antibarcerial; antifungal; anticheumatic; antibarcerial; antifungal; anticheumatic; antichyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cadiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autonimune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartillage; damage; antinflammatory disease; coagulation;
leukaemia comprising a mouse having defective nor-1 and nur77 nucleic
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                          ;
                                                            Sequence 5115 BP; 1417 A; 1196 C; 1089 G; 1412 T; 0 U; 1 Other;
                                                                                                     Length 5115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ORFX ORF3017 polynucleotide sequence SEQ ID NO:6033.
                                                                                                                                            Indels
                                                                                                   DB 10;
                                                                                                   Score 16.8; DB 1 Pred. No. 2e+02;
                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                        4908 GCTGTTAATGGAGAGTGCCT 4927
                                                                                                                                                                                   1 GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                             AAC77462 standard; cDNA; 5157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thrombosis; contraceptive; ss.
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99US-0127636P.
99US-0127728P.
                                                                                                   84.0%;
90.0%;
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                                                                                                                      Local Similarity 90.0
es 18; Conservative
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P-PSDB; AAB43253.
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                     acid sequences.
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02-APR-1999;
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                                                                                                     Query Match
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                         to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyridism, cholesterol ester storage, systemic lupus erychematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal heamoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive
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   sequences can be used for determining the presence of or predisposition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 3; Length 5157; 90.0%; Pred. No. 2e+02; ive 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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P-PSDB; AAY02377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal sequence trap method; SST method; immunisation; inhibition; infection; allergy; cancer; regulation; tissue formation; tissue repair; activin activity; inhibin activity; dhemokine activity; cytokine activity; blood coagulation regulation; agonist; antagonist; metabolic disorder; hormonal disorder; immune disorder; severe combined immunodeficiency; SCID; AIDS; thrombosls; cancer; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides identified by the signal sequence trap method from a human cDNA library.
viruses (including HIV) and protozoa; metabolic and hormonal disorders; immune disorders (including severe combined immunodeficiency (SCID) and AIDS; thrombosis; cancer; and traumatic or surgical wounds
                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA encoding a protein identified by the signal sequence trap method.
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                                                                           1470 A; 1204 C; 1128 G; 1376 T; 0 U; 0 Other;
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                                                                                                             84.0%; Score 16.8; DB 2; Length 5178; 90.0%; Pred. No. 2e+02; .ive 0; Mismatches 2; Indels 0;
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Pred. No. 2.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                 3291 GCAGTCAATGGAGAATGGCT 3310
                                                                                                                                                                                           GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                                                                                                             AAX35733 standard; cDNA; 5457 BP.
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Best Local Similarity 90.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                               Query Match
Best Local Similarity 90.0'
Matches 18; Conservative
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                                                                               Sequence 5178 BP;
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                                                                                                                                                                                                                                                                                         RESULT 18
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

30-MAR-2001; 2001WO-US008631

WO200175067-A2 Homo sapiens.

11-OCT-2001.

DNA encoding novel human diagnostic protein #1463.

13-FEB-2002 (first entry)

AAS65659;

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T cell; gene; ss; differential expression; T cell activation; antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy; allergy; cancer; graft versus host disease; infection; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New combination comprising several cDNAs that are differentially expressed in activated T cells, useful for diagnosing, treating, staging or monitoring treatment for allergy, cancer, infectious and/or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to the sequences of several cDNAs that are differentially expressed in activated T cells. The sequences of the invention may have antiallergic, cytostatic, immunosuppressive and antimicrobial activity and may be used in gene therapy. The invention also comprises a method for screening samples for differentially expressed genes and a method for detecting these cDNAs by hybridisation. The methods and compositions of the present invention are useful for diagnosing, treating, staging or monitoring treatment for allergy, disorders. The present sequence represents a cDNA of the invention that is differentially expressed in activated T cells
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                             3298 GCAGTCAATGGAGAATGGCT 3317
GCAGTTAATGGAGAGTGGCT 20
                                                                                                                   ABX62937 standard; cDNA; 5642 BP.
                                                                                                                                                                                                                        Human activated T cell cDNA #53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page; 180pp; English.
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Best Local Similarity 90.0
Matches 18; Conservative
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(PETE/) PETERSON D P.
(COCK/) COCKS B G.
(HAWK/) HAWKINS P R.
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                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supperfue in tissue, as molecular weight markers and as a food of stees expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on but and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5768 BP; 1592 A; 1319 C; 1284 G; 1572 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1463; 103pp; English.
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P-PSDB; ABG01472.
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5472 GCTGTTAATGGAGAGTGCCT 5491

1 GCAGTTAATGGAGAGTGGCT 20

AAS65659 standard; cDNA; 5768 BP.

RESULT 20 AAS65659 ID AAS65

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The invention relates to a combination comprising several polymucleotides calmedulin gene, human mRNA for KIRA4030 protein, leakotriene A4 hydrolase, human CGI-142 protein mRNA, human X+ channel beat 2 subunit can be their complements. The cDNAs are differentially expressed in LPS (lipopolysaccharide)-treated foam cells. Also included are obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, and ADE25751, producing a protein by culturing the host cell, and a composition comprising a protein by culturing the host cell, and a composition comprising a protein by culturing the host cell, and a composition comprising a protein by culturing the host cell, and a composition comprising a protein by culturing the most cell, and a composition comprising a protein action are useful for a high throughput screening of a library of molecules or compounds to differential expressed nucleic acids are useful for high throughput screening of a library of molecules or compounds to identify a ligand which binds a polynuclectide. The library is chosen content for a high throughput screening of library of molecules or compounds to useful for a high throughput screening of library of molecules or compounds to identify at least one ligand which specifically binds a compounds to identify at least one ligand which specifically binds a protein setul for main diagnosing a protein for main and long and antibody. The form cell-expressed nucleic acids are useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foam cell-expressed nucleic acids are useful for diagnosing cardiovascular disorder. The foam cell-expressed nucleic acids are useful as elements on a microarray which can be used for detecting related polynucleotide in a sample, diagnosing cardiovascular disease,
                                                                                                        Human; ss; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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                                                                   Human cDNA differentially expressed in foam cells #105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaser MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 105; 37pp; English.
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                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001; 2001US-0323784P.
                                                                                                                                                                                                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
                        (first entry)
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                                                                                                                                                                                                                                     JS2003194721-A1.
                                                                                                                                                                                        Homo sapiens.
                      29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mikita T,
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atherosclerosis. The present sequence represents a cDNA whose expression is upregulated in LPS treated foam cells.
                                                                                                                                                Sequence 5828 BP; 1535 A; 1422 C; 1242 G; 1534 T; 0 U; 95 Other;
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Matches

5021/c AAS65021 standard; cDNA; 6092 BP. RESULT 22 AAS65021/c ID AAS65

(first entry) 13-FEB-2002 ONA encoding novel human diagnostic protein #825.

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

Tang YT; Liu C, Drmanac RT,

WPI; 2001-639362/73. P-PSDB; ABG00834.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 1; SEQ ID NO 825; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) is useful in gene therapy techniques to restore normal control in its useful in gene therapy techniques to restore normal control in its useful in gene therapy techniques to restore normal consequity of (II) of (III) of (IIII) of (III) of ( slectronic format directly from WIPO at ttp.wipo.int/pub/published\_pct\_sequences 

Sequence 6092 BP; 1677 A; 1318 C; 1389 G; 1708 T; 0 U; 0 Other;

Gaps ; Length 6092; Indels Match 84.0%; Score 16.8; DB 5; Local Similarity 90.0%; Pred. No. 2.1e+02; les 18; Conservative 0; Mismatches 2; Query Match Matches

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AAS66214 standard; cDNA; 6291 BP. RESULT 23
AAS66214
ID AAS66
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AC AAS66

AAS66214;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in some therapy reciping or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating or polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations are responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and among a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the products dependent on DNA and and a managed to the product of the products dependent on DNA and and a managed to the product of the products dependent on DNA and and a managed to the product of 
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                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                  DNA encoding novel human diagnostic protein #2018.
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23-AUG-2000; 2000US-00649167.
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                              13-FEB-2002 (first entry)
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P-PSDB; ABG02027.
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                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                            Human;
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ACC72047
ID ACC72:
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DT 08-JU
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Tang YT;

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New isolated human differentially-regulated breast cancer polynucleotide and polypeptide, useful for diagnosing, staging, prognosticating, preventing and/or treating diseases and conditions relating to breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SET; PN12218; TTP; CIN85; PN13734; TIAR; FUBP1; antiinflammatory;
antiarteriosclerotic; cardiant; nootropic; gene therapy; gene; human; ds.
                                            Breast cancer, cytostatic, gene therapy; antisense therapy; regulated; drug discovery, clinical medicine, forensic medicine, gene; chromosome 16q13; ds.
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162. .6587
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                                                                                                                                                                                                                                                                                          (ORIG-) ORIGENE TECHNOLOGIES INC.
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14-MAY-2002; 2002US-00144194.
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             BCU0586 gene #SEQ ID 71.
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Best Local Similarity
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                                                                                                                                           WO2003029421-A2
                                                                                                              Homo sapiens,
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2000US-0224518P.
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08-SEP-2000; 2
12-SEP-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated protein complex comprising 2 proteins. The protein complex comprises: (a) a first protein (P1) and a second protein (P2); (b) a fragment P1 and P2; (c) P1 and a fragment P2; and (d) a fragment of P1 and a fragment P2. The first and a fragment P2 is of the complex are selected from: (i) P1 is SET, and P2 is PN12218; (ii) P1 is TTP and P2 is CN85 or PN13734; or (iii) P1 is TAR and P2 is FN12218; (ii) P1 is TTP and P2 is CN85 or PN13734; or (iii) P1 is TAR and P2 is FUBP1. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of physiological disorders involved in the protein-protein interaction, such as inflammatory disease, modulators, inhibitor or compounds are useful for treating the diseases described above. The present sequence represents the nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid archritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ds; acquired immune deficiency syndrome.
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                                                                                                                                                                                                                                                                                                      New isolated protein complex comprising a first and second protein, useful for the diagnosis and treatment of disorders involved in the protein-protein interaction, such as inflammatory disease, atherosclerosis or hypoxic brain injury.
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 123; Page 21-23; 77pp; English.
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P-PSDB; ABB81196.
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Ruben SM;

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The invention relates to novel isolated polypeptides (I), and display to (I). (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. congenital and acquired immunodeficiencies, autoimmune creations and graft versus host disease, infectious diseases (reg. pepatitis C), bleeding disorders, haemoglobin abnormalities and cher blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. disease, adisease), chromosomal abnormalities and disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher disease, Parkinson's disease), chromosomal abnormalities (c.g. Lown syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. disease), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (e.g. Addison's disease), reproductive system disorders, gastroinesstinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce (inflammatory disorders) index ameans to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27880 represent novel signal transduction pathway protein coding sequences and PCR primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antinflammatory; anti-HIV; antibacterial; antinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AlDS; ds; acquired immune deficiency syndrome.
                                                                  Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.
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                                                                                                                                                                   Claim 1; SEQ ID NO 1313; 880pp; English.
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AAS27652 standard; DNA; 29220 BP.
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GENOME HUMAN (HUMA-)

SM Ruben Barash SC, CA, Rosen

2001-465460/50

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders.

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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune traplations and graft versus host disease, infectious diseases (ransplant relections and graft versus host disease, infectious diseases (e.g. traplations and graft versus host disease, infectious diseases (e.g. traplations and graft versus host disease, infectious diseases (e.g. disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease, Parkinson's disease), reproductive disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (C.g. Jomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders (in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, garrhythmia, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce (inflammatory disorders), liver disorders (cirrhosis), as stimulators of higher affinity antibodies, and as a means to oi induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction pathway protein coding
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Claim 1; SEQ ID NO 1312; 880pp; English.
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04-FEB-2000;
28-JUN-2000;
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological sample and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide is also useful for identifying a binding partner and determining whether the binding partner or othe polypeptide is also useful for identifying a binding partner and determining whether the binding partner or acid enceding the polypeptide is useful for preventing, treating, or acid enceding the polypeptide is useful for preventing, treating or ameliorating a medical condition, which involves administering the polypeptide or the nucleic acid to a mammalian subject. The nucleic acid can use useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, which involves determining the presence or absence of a mutation in The nucleic acid, and diagnosing a pathological condition or susceptibility to a pathological condition or susceptibility 
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                                        2000US-0226868P.
2000US-0228924P.
2000US-0229287P.
2000US-0229343P.
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2000US-0234274F.
2000US-0234997F.
2000US-0225758P.
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2000US-0229345P.
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2000US-0236327P.
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2000US-0236369P.
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2000US-0237037P.
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(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                                        05-SEP-2000;
05-SEP-2000;
08-SEP-2000;
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27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0236327P.
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29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236368P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237039P.
03-OCT-2000; 2000US-023993FP.
03-OCT-2000; 2000US-024080P.
01-NOV-2000; 2000US-024080P.
01-NOV-2000; 2000US-024080P.
03-DEC-2000; 2000US-024980P.

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the nucleic acid and the antibody are useful as immunosuppressive agents, as a adjuvants to enhance elegences, and as agents to induce higher affinity antibodies and increase serum immunoglobulin concentrations. The present sequence represents DNA encoding a novel human protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format direct from USPTO at seqdata.uspto.gov/sequence.html?DocID=20020168711.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; gene; human; autoimmune disease; Parkinson's disease; silicosis; gastrointestinal disease; atherosclerosis; haemophilia; thrombocytopenia; fimunosuppressive agent; adjuvanti, enhance immune response; higher affinity antibody induction; increased serum immunoglobulin concentration.
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                                                                                                                                                                                                                   Sequence 29220 BP; 8660 A; 6345 C; 6354 G; 7861 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                Query Match

84.0%; Score 16.8; DB 10; Length 29220;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                        ADB94456 standard; DNA; 29220 BP
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28-UW-2000; 2000US-01180628P.
07-JUL-2000; 2000US-0216880P.
11-JUL-2000; 2000US-0216880P.
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11-JUC-2000; 2000US-022944P.
11-JUC-2000; 2000US-0229344P.
11-JUC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human protein DNA #65.
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The invention relates to an isolated polypeptide. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject, by determining the presence or amount of expression of the polypeptide in a biological semple and diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the condition based on the presence or amount of expression of the perpetide. The polypeptide is also useful for identifying a binding partner to the polypeptide which involves concacting the polypeptide or the polypeptide is useful for preventing the polypeptide or the nucleic acid encoding the polypeptide; The polypeptide or the nucleic acid encoding the polypeptide is useful for preventing the polypeptide or the nucleic acid encoding a medical condition, which involves administraing the polypeptide or the nucleic acid to a pathological condition or a susceptibility to a pathological condition or a susceptibility to a pathological condition or susceptibility to a pathological condition or susceptibility to a pathological condition or based on the presence or absence of the mutation. The polypeptide, the nucleic acid and an antibody to the polypeptide are useful for treating disease, atherosclerosis, haemophilia, thrombocytopenia. The polypeptide of the nucleic acid and the antibody are useful as immunosuppressive agents, as adjuvants to enhance immune responses, and as agents to induce higher affinity antibodies and increase serum immunosuppressive acid and the antibody are useful as immunosuppressive account and the antibody are useful as agents to induce higher expressive pathological conditions and increase serum immunosuppressive the processive and as agents to induce the sequence data for this patent did not form part of the prince for
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Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
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(BARA/) BARASH S C.
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in 255h6"
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/tag= b
1126. .1220

/noce= "MIR repeat family"

replace (1128, T)
/tag= putative polymorphism, C in 52b3, T in pbJ84g1S"

replace (1909, C)
/tag= "putative polymorphism, A in 52b3, C in pbJ84g1S"

replace (1920, T)
/tag= complement (2310. .2482)

/tag= putative polymorphism, C in 52b3, T in pbJ84g1S"

replace (1920, T)
/tag= putative polymorphism, C in 52b3, T in pbJ84g1S"
/tag= complement (2310. .2482)
                                                                                                                                         Tumour suppressor gene; chromosome 6q27; cancer; therapy; human; D68297; breast cancer; ovarian cancer; lymphoid cancer; marker; D6S193; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               /*täg= g
2749. .2843
/*tag= h
replace(2984,T)
/*tag= "putative polymorphism, C in 52b3, T in pDJ84g15"
complement(3083. .3201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= n
4878. 4927
/*tag= n
4912. 5093
/*tag= p
complement(5398. .5563)
/*tag= match: D6S193 microsatellite"
                                                                                                                    Human chromosome 6q27 tumour suppressor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= u
/note= "trapped exon"
complement (6887, .6892)
/*tag= w
complement (7237, .7434)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               '*tag= k
complement(4483. .4532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tåg= 1
:omplement(4615. .4664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= t
complement(6395. .6456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= v
complement(6395. .6438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= j
note= "trapped exon"
                                                AAX57351 standard; DNA; 68940 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= r
5767. .5816
/*tag= s
6072. .6134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= m
4854. .4903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3793
                                                                                             16-AUG-1999 (first entry)
                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                       polyA_site
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                                                                       AAX57351;
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                                                                                                                                                                                                                                                                                                                                                                                                      exon
                           RESULT 30
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AAKS6733 04/c

ContinuaTion (5 of 15) of AAK96733 from base 400001 (Human neuregulin-1 gene.)

WP Sequence split into 15 fragments LOCUS AAK96733 Accession Aak86733

WP AAK96733_00

WP AAK96733_01 100001 110000

WP AAK96733 03 300001 410000

WP AAK96733 04 400001 510000

WP AAK96733 05 600001 7100000

WP AAK96733 06 600001 7100000

WP AAK96733 09 800001 1010000

WP AAK96733 09 900001 1010000

WP AAK96733 10 1000001 1110000

WP AAK96733 11 1100001 1310000

WP AAK96733 11 1100001 1310000
                                                                                                                                                                                                                                                                                                                          of AAK95240 from base 800001 (Human neuregulin-1 gene.)

15 fragments LOCUS AAK95240 Accession Aak95240

Begin End
100001 210000
200001 310000
300001 510000
500001 510000
500001 710000
500001 710000
800001 1010000
900001 1010000
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                                                                                                                                                                                            Score 16.8; DB 4; Length 110000;
Pred. No. 3.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16.8; DB 4; Length 110000;
Pred. No. 3.2e+02;
0; Mismatches 2; Indels 0;
110000
310000
410000
610000
110000
1110000
1110000
1110000
1110000
1110000
1110000
1110000
1110000
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1310000
1410000
                                                                                                                                                                                                                                            84771 GCAGGTAATGGAGAGTGCCT 84752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%;
90.0%;
                                                                                                                                                                                             84.0%;
90.0%;
          100001
200001
300001
500001
600001
700001
1000001
1100001
1300001
1400001
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1200001
1300001
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Best Local Similarity 90..
Best Local Similarity
These 18; Conservative
                                                                                                                                                                                                       Local Similarity 90.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                               0f
15
                                                                                                                                                                                                                                                                                                      RESULT 32
AAK95240 08/C
Continuation (9 of 15) of
WP Sequence split into 119
WP Fragment Name
AAK92240 00
WP AAK92240 01
WP AAK92240 02
WP AAK92240 05
WP AAK92240 05
WP AAK92240 05
WP AAK92240 06
WP AAK92240 06
WP AAK92240 06
WP AAK92240 07
WP AAK92240 08
WP AAK92240 11
WP AAK92240 11
WP AAK92240 11
AAX95240_00
AAK95240_01
AAX95240_02
AAX55240_03
AAX55240_04
AAX55240_06
AAX55240_07
                                                                                                                                                                                                Query Match
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Matches
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AAK55240 04/c

Continuation (5 of 15) of AAK95240 from base 400001 (Human neuregulin-1 gene.)

WP Sequence split into 15 fragments LOCUS AAK95240 Accession Aak95240

WP Fragment Name Begin End
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                     /*tag= bd
//*tag= bd
//*tag= bd
/*tag= be
/*tag= be
/*tag= bt
/*tag= bt
/*tag= bt
/*tag= bt
/*tag= bt
//*tag= bi
                                                                                                                                                                                                                                                                                                                                            /*tag= bo
/note= "putative polymorphism (T)5 in pDJ84g15"
complement(24244. .24293)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 84.0%; Score 16.8; DB 2; Length 68940;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= by
/note= "TIGGER2 repeat family"
complement(34879. .35035)
                                                                                                                                                                                                                                                                                                                               replace(24182. .24186, TTTTT)
                                                                                                                                                                                                                                                                                                                                                                              /*tag= bp
24266. 24315
/*tag= bg
/*tag= br
/*tag= br
30550. 31665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= bw
/note= "Alu repeat family'
complement(33782. .33867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= ca
/note= "trapped exon"
complement(34879, .34941)
                                                                                                                                                                                                                                              /*tag= bk
22856. .22956
/*tag= bl
complement(23196. .23233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= bx
complement(34638. .34996)
/*tag= bc
complement(19541. .19683)
                                                                                                                                                                                                                                                                                             /*tag= bm
complement(23288. .23293)
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32483. 32488
/*tag= bu
32483. 32488
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35223. .35327
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= bs
30550. .30863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= bv
33639. .33870
                                                                                                                                                                                                                                                                                                                     /*tag= bn
                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
               repeat_region
                                                  repeat_region
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of
15
ABT00010 08/C
Continuation (9 of 15) of
WP Sequence split into 15
WP ABT00010 00
WP ABT00010 03
WP ABT00010 03
WP ABT00010 04
WP ABT00010 06
WP ABT00010 06
WP ABT00010 06
WP ABT00010 06
WP ABT00010 09
WP ABT00010 09
WP ABT00010 09
WP ABT00010 09
WP ABT00010 12
WP ABT00010 12
WP ABT00010 11
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 35
ABTO0010_04/c
Continuation (5 of 15) of ABT00010 from base 400001 (Human neuregulin 1 gene.)
WP Sequence split into 15 fragments LOCUS ABT00010 Accession Abt00010
WP Fragment Name Begin End 110000
WP ABT00010_01 100001 310000
WP ABT00010_03 300001 410000
WP ABT00010_04 400001 510000
WP ABT00010_05 500001 610000
WP ABT00010_06 600001 710000
WP ABT00010_06 600001 100000
WP ABT00010_07 800001 1100000
WP ABT00010_07 100001 1100000
WP ABT00010_01 1100001 1210000
WP ABT00010_10 1100001 1210000
WP ABT00010_11 1100001 1210000
WP ABT00010_12 1200001 1210000
WP ABT00010_12 1200001 1503841
                                                                                    ö
                                                                                                                                                                                                                                  from base 800001 (Human neuregulin-1 gene. )
  LOCUS AAK96733 Accession Aak96733
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                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                    Score 16.8; DB 4; Length 110000; Pred. No. 3.2e+02; ); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 6; Length 110000;
Pred. No. 3.2e+02;
); Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.8; DB 4;
Pred. No. 3.2e+02;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                  910000
1010000
1110000
1210000
1310000
1503900
     1410000
1503900
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210000
310000
410000
510000
610000
810000
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                                                                                                                                                   53558 GCAAGTAATGGAGAGTGGCT 53539
                                                                                                                                                                                                                AAK66733 08/C
Continuation (9 of 15) of AAK96733 from
WP Sequence split into 15 fragments LG
WP Fragment Name Begin 111
WP AAK96733 00 100001 21
WP AAK96733 01 200001 31
WP AAK96733 04 400001 31
WP AAK96733 04 400001 31
WP AAK96733 06 600001 61
WP AAK96733 06 600001 61
WP AAK96733 06 600001 91
WP AAK96733 09 900001 101
WP AAK96733 10 1000001 111
WP AAK96733 10 1000001 111
WP AAK96733 11 1100001 1210
WP AAK96733 11 1100001 1210
WP AAK96733 12 1200001 1310
WP AAK96733 12 1200001 1310
WP AAK96733 13 13 1300001 1310
WP AAK96733 14 1400001 1503
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0
                                                                                                                     1 GCAGTTAATGGAGAGTGGCT
     1300001
                                                    Query Match,
Best Local Similarity 90.0%;
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.06;
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Conservative
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Best Local Similarity
Matches 18; Conserv
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les 18; Conserv
   AAK96733_13
AAK96733_14
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Matches
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RESULT 36

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RESULT 37
APTO1503 04/C
Continuation (5 of 15) of ABT01503 from base 400001 (Human neuregulin 1 gene.)
WP Sequence split into 15 fragments Locus ABT01503 Accession Abt01503
WP ABT01503 00 100001 210000
WP ABT01503 00 100001 310000
WP ABT01503 00 100001 310000
WP ABT01503 00 100001 100000
WP ABT01503 00 500001 510000
WP ABT01503 00 500001 100000
WP ABT01503 00 1000001 1100000
WP ABT01503 00 1000001 1100000
WP ABT01503 01 1000001 1100000
WP ABT01503 01 1000001 1100000
WP ABT01503 11 1100001 1110000
WP ABT01503 11 1100001 11310000
WP ABT01503 11 1100001 11503011 11503001
WP ABT01503 11 1100001 11503011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from base 800001 (Human neuregulin 1 gene. ) LOCUS ABT00010 Accession Abt00010
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                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 110000;
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0
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                                                                                                                                                                                                                                                     Score 16.8; DB 6;
Pred. No. 3.2e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 16.8; DB 6;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.26
; Mismatches
                                       110000
310000
410000
410000
510000
710000
1110000
1110000
1110000
11110000
11110000
11110000
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  ABT00010 f.
fragments
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCAGTIAATGGAGAGTGGCT
                                                    100001
200001
4000001
500001
600001
800001
1100001
11200001
1400001
                                                                                                                                                                                                                                                       84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%;
90.0%;
                              Begin
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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84772 GCAGGTAATGGAGAGTGCCT 84753

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g à

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The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sample indicates the cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences and be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                    soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 158811 BP; 50626 A; 28156 C; 29409 G; 50620 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 15811; Score 16.8; DB 12; Length 158811; Local Similarity 90.0%; Pred. No. 3.4e+02; les 18; Conservative 0; Mismatches 2; Indels 0; C
                                                                                                                                                                     Human soft tissue sarcoma-upregulated DNA - SEQ ID 2720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of the human musashi promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; SEQ ID NO 2720; 210pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                         (PRCT-) PROTEIN DESIGN LABS INC.
                                                           ADQ19901/c
ID ADQ19901 standard; DNA; 158811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH28355 standard; DNA; 52216
                                                                                                                                                                                                                                                                                                                                                                                         26-NOV-2002; 2002US-0429739P.
                                                                                                                                                                                                                                                                                                                                                          26-NOV-2003; 2003WO-US038193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-SEP-2001 (first entry)
                                                                                                                                         26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aziz N, Ginsburg WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-441208/41
                                                                                                                                                                                                                                                                                          WO2004048938-A2.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                           10-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH28355;
                                                                                                           ADQ19901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH28355
ID AAH2
XX
AC AAH2
XX
DT 05-S
XX
DE Nucl
                                           RESULT 41
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                                                                                                                                                                                                                                                                                             gene. )
                                                                                                                                                                                                                                                          RESULT 39

ADH77486 O4/c

Continuation (5 of 15) of ADH77486 from base 400001 (Human neuregulin gene.

WP Sequence split into 15 fragments LOCUS ADH77486 Accession Adh77486

WP ADH77486 00 100001

WP ADH77486 01 200000

WP ADH77486 02 300001 410000

WP ADH77486 04 40001 510000

WP ADH77486 05 600001 710000

WP ADH77486 05 600001 100000

WP ADH77486 07 700001 100000

WP ADH77486 09 900001 1100000

WP ADH77486 10 1000001 1100000

WP ADH77486 10 1000001 1100000

WP ADH77486 11 1100001 1310000

WP ADH77486 11 1100001 14100000

WP ADH77486 11 1100001 1503841
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                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 12; Length 110000; 90.0%; Pred. No. 3.2e+02; ive 0; Mismatches 2; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 110000;
                                                                                                          Score 16.8; DB 6; Length 110000;
Pred. No. 3.2e+02;
0; Mismatches 2; Indels 0;
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Pred. No. 3.2e+02;
0; Mismatches 2;
1010000
1110000
1210000
1310000
1410000
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210000
310000
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                                                                                                                                                                                                 84772 GCAGGTAATGGAGAGTGCCT 84753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGTTAATGGAGAGTGGCT 20
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                                                                                                                                                                               1 GCAGTTAATGGAGAGTGGCT 20
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fragments
Begin E
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                               84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200001
300001
400001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              500001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700001
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900001
1000001
1100001
1200001
1400001
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                                                                                                                                                Conservative
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15
                                                                                               Query Match
Best Local Similarity
-hea 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 40
ADH77486 08/C
Continuation (9 of 15) of
WP Sequence split into 15
WP Fragment Name
WP ADH77486 00
WP ADH77486 01
WP ADH77486 02
WP ADH77486 05
WP ADH77486 05
WP ADH77486 06
WP ADH77486 06
WP ADH77486 07
WP ADH77486 10
WP ADH77486 10
WP ADH77486 10
WP ADH77486 11
WP ADH77486 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
ABT01503_09
ABT01503_10
ABT01503_11
ABT01503_12
ABT01503_13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
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Best Loc Matches

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Gaps

99US-0173003P

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engraftment characteristics. The cells are useful in support of the structural repair of the damaged central nervous system, such as in the traumatized brain, or the contoured, traumatized or transected spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52216 BP; 13494 A; 12461 C; 12362 G; 13899 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 82.0%; Score 16.4; DB 4; Length 52216; Best Local Similarity 94.4%; Pred. No. 4.6e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
         Musashi promoter; multipotential neural progenitor cell; neural stem cell; central nervous system; ss.
                                                                                                                                   (CORR ) CORNELL RES FOUND INC.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                            Claim 12; Fig 11A-JJ; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21276 GCAGTTAGTGGAGAGTGG 21293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL50307 standard; DNA; 52216 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GCAGTTAATGGAGAGTGG 18
                                                                                              22-DEC-2000; 2000WO-US035395.
                                                                                                                                                                Goldman SA, Okano H;
                                                                                                                                                                                   WPI; 2001-418053/44.
                                                        WO200146384-A2
                                      Homo sapiens,
                                                                                                                23-DEC-1999;
                                                                           28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL50307;
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The present invention describes a method for separating multipotential neural progenitor cells from a mixed population of cell types in which a promoter functioning selectively in the neural progenitor cells is selected. A nucleic acid molecule encoding a fluorescent protein is introduced to all cell types of the mixed population of cell types under control of the promoter. Only the neural progenitor cells (not the other mixed population of cell types that are fluorescent protein, cells of the mixed population of cell types that are fluorescent, which are restricted to the neural progenitor cells, are identified. The fluorescent cells are separated from the mixed population of cell types, the separated cells are are restricted to the neural progenitor cells. The present invention also describes: (1) an isolated human masship promoter, and (2) an enriched or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purified preparation of isolated multipotential neural progenitor cells. The method is used for separating multipotential neural progenitor cells from a mixed population of cell types. The present sequence represents the human musashi promoter DNA sequence which can be used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation and purification of multipotential neural progenitor cells and multipotential neural progenitor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52216 BP; 13494 A; 12460 C; 12362 G; 13900 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glutamate N-methyl-D-aspartate receptor; neurodegenerative disease; stroke, Alzhaimer, disease, parkinson's disease, pain, myopathy; noctropic; neuroprotective; cerebroprotective; antiparkinsonian; analgesic; diagnosis; gene therapy; screening; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine racemase; human; D-serine; regulation;
                                                                                                                                                                                                                                   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 29; Page 14-31; 123pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human serine racemase PCR primer B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21276 GCAGTTAGTGGAGAGTGG 21293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GCAGTTAATGGAGAGTGG 18
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                                                                           05-JAN-2001; 2001JP-0000868
                                                                                                                                                       35-JAN-2000; 2000JP-00005307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Conservative
                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-275726/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200173077-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
05-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2001.
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XX
AC AAI70
XX
DT 21-JJ
XX
XX
DE Human
XX
XW SCTII
XW S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the human musashi promoter, which is used in the method of the invention. The specification describes a method for separating multipotential neural progenitor cells from a mixed population of cell types. The method comprises introducing a nucleic acid encoding a fluorescent protein under control of a promoter which selectively functions in the progenitor cells, into all cell types of the mixed population, allowing only the progenitor cells to express the fluorescent protein, and identifying and separating cells that are fluorescent where the separated cells are progenitor cells. The method is useful for isolation and purification of multipotential neural progenitor cells, especially neural stem cells from adult brain. The isolated cells are used in both basic analyses of precursor and stem cell growth control, as well as in more applied studies of their transplantability and control, as well as in more applied studies of their transplantability and control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Separating multipotential neural progenitor cells from a mixed population of cells, involves introducing nucleic acid molecule encoding fluorescent protein under promoter control, and separating fluorescent cells.
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(FARB ) BAYER AG

Human musashi promoter DNA sequence SEQ ID NO:1.

JP2002034580-A.

Homo sapiens

(first entry)

13-JUN-2002

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Example 2; Page 51; 66pp; English
                                                                                                                       Query Match
Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
                                                                                                                                                                                                                                                    18-JAN-2000; 2000WO-US000938
                                                                                                                                                                       AAA59296 standard; DNA; 509
                                                                                                       the glutamate NMDA receptor
                                                                                                                                                                                                                                                                                                    WPI; 2000-482915/42.
            WPI; 2001-648444/74
    Ramakrishnan S;
                                                                                                                                                                                                                                    WO200043526-A1
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                             19-JAN-1999;
                                                                                                                                                                                                                                                                  21-JUL-1999;
                                                                                                                                                                                        07-NOV-2000
                                                                                                                                                                                                                                            27-JUL-2000
                                                                                                                                                                                                                                                                                        Snyder SH,
Ferris CD;
                                                                                                                                                                               AAA59296;
                                                                                                                                                                                                                                                                                            Ferris
                                                                                                                                                               RESULT 45
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The present sequence represents a fragment of a mammalian serine racemase gene. The racemase polypeptide has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspareate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspareate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone disease and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding serine racemase enzyme and the enzyme useful for screening reagents regulating the activity of the enzyme in a neuron disease caused by over- or under-activation of glutamate N-methyl-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of cDNA encoding human serine racemase (see AAM50262). The polynucleotide can be used in the production of recombinant serine racemase enzyme, or for the detection of serine
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutamate N-methyl-D-apartate receptor; neurodegenerative disease; stroke; Alzheimer's disease; Parkinson's disease; pain; myopathy; nootropic; neuroprotective; cerebroprotective; antiparkinsonian; analgesic; diagnosis; gene therapy; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 3; Length 509;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                        Sequence 509 BP; 139 A; 90 C; 115 G; 164 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        racemase; human; D-serine; regulation;
                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
52. .1074
/*tag= a
                                                                                                                                                                                                                                                                                                                                     80.0%; Scu-
100.0%; Pred
0; N
                Claim 18; Page 27; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI70575 standard; cDNA; 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0193748P.
03-APR-2000; 2000US-0194249P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-EP003668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human serine racemase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-648444/74.
P-PSDB; AAMS0262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2002
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                                                                                                                                                                                                                                                                The present sequence is that of primer B, designed for use with primer A (see AAI70576) in the PCR amplification of human serine racemase CDNA (see AAI70575). The expected size of the specific PCR product is 536 bp. Human cDNA phage libraries were used as templates in PCR analysis in order to determine the expression pattern of serine racemase mRNA in human tissue. The invention provides methods of regulating serine racemase activity in order to increase or decrease Duranting serine formation, and thereby increase or decrease glutamate N-methyl-D-aspartate (NMDA) receptor activation. A decrease glutamate N-methyl-D-aspartate (NMDA) receptor activation. A decrease in D-serine formation may aid in the Regulation of neuron damage following an ischaemic event, such as stroke. Regulation of D-serine formation may also aid in the treatment of other neurodegenerative conditions caused by the over- or under-activation of
                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                           Polynucleotide encoding serine racemase enzyme and the enzyme useful screening reagents regulating the activity of the enzyme in a neuron disease caused by over- or under-activation of glutamate N-methyl-D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 4; Length 29;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29 BP; 10 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal sequence of human serine racemase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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99US-0144839P.
99US-0145953P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 TTAATGGAGAGTGGCT 20
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Novel polypeptide of the human pyridoxal phosphate dependent family useful in screening and detection assays and for treatment, e.g. of epilepsy and Alzheimer's.

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racemase polynucleotides. Expression vectors and host cells are claimed
                                                                                                                                                           WO200160987-A1
                                                                                                                              Homo sapiens
                                                                                                                                              misc_feature
                                                                                                                                                                 23-AUG-2001
                                                                                                                                                                                      feyers RA,
                                                                                        AAD14461;
                                                     Query Match
Best Local 9
                                                                             Matches
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damage following various nervous system diseases is often caused by activation of glutamate N-methyl-D-asparate (NMDA) receptors in the brain. This receptor is activated by the binding of D-serine. Requlation of D-serine levels through regulation of serine racemase may therefore prevent or minimise neuron of serine racemase may therefore neurodegenerative disorders such as Alzheimer's disease and parkinson's disease, and disorders such as Alzheimer's disease and Parkinson's cacemase polypeptides and polymolectides are used in claimed methods of screening for agents that modulate or decrease the activity of serine racemase. Also claimed is a pharmaceutical composition comprising either an expression vector that contains a serine racemase polymuclectide, or a cagent that modulates serine racemase polymuclectide, or a modulate serine racemase enzyme activity. This is used to modulate serine racemase enzyme activity. This is used to damage or a neurodegenerative disease caused by the over- or under-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16; DB 4; Length 1336; 100.0%; Pred. No. 4.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1336 BP; 386 A; 268 C; 319 G; 362 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activation of the glutamate NMDA receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50
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ö Human; pyridoxal phosphate dependent enzyme; nootropic; neuroprotective; Human pyridoxal-phosphate dependent enzyme 22406 cDNA. 1166 TTAATGGAGAGTGGCT 1181 AAD14461 standard; cDNA; 1770 15-NOV-2001 (first entry)

anticonvulsant; cerbroprotective; cardiant; vasotropic; gene therapy; epilepsy; Alzheimer's disease; chromosome 17; serine racemase; stroke; behavioural change; neurodegenerative disorder; schizophrenia; atresia; rheumatic heart failure; circulatory disorder; hepatic injury; jaundice; lung disorder; nodular hyperplasia; stenosis; skeletal muscle disorder; tumour; rhabdomyosarcoma; dermal fibroblast disorder; ss.

/\*tag= b /note= "This region is specifically claimed as SED ID NO: /product= "Human pyridoxal phosphate dependent enzyme" 59. .1088 location/Qualifiers in claim 1" /\*tag= a .1091

Denign prostatic hypertrophy; systemic lupus erythematosus; cardiant; hepatotropic; virucide; cytostatic; cerebroprotective; nootropic; neuroprotective; anticonvulsant; antiinflammatory; immunosuppressive;

17-FEB-2000; 2000US-0183208P. (MILL-) MILLENNIUM PHARM INC. 20-FEB-2001; 2001WO-US005365 Rudolph-Owen LA; WPI; 2001-529909/58. P-PSDB; AAE08342.

2000US-0219140P 2000US-0229465P 2000US-0253878P 2000US-0250338P 2000US-0250338P

20-JUL-2000; 20-JUL-2000; 29-NOV-2000;

30-NOV-2000; 30-NOV-2000; 30-NOV-2000;

07-JUN-2002; 2002US-00164966

US2003064439-A1.

03-APR-2003

Homo sapiens

gene; ss

2000US-0183208P

17-FEB-2000; 26-JUN-2000;

The present sequence is a cDNA encoding human pyridoxal phosphate dependent enzyme 22406 which is a serine racemase. Human 22406 gene is located on chromosome 17 between D17849 and D178796. The protein 22406 is a modulator of D-serine. D serine has been shown to modify behavioural changes associated with learning, memory and convolsions. Human 22046 and diagnose neurodegenerative discorders including Alzheimer's disease, schizophrenia as well as quell anxiety and epilepsy and prevent damage from stroke as well as quell anxiety and epilepsy and prevent damage from stroke as well as cardiac (heart failure, rheumatic heart failure) and circulatory disorders, liver disorders (heaptic injury, jaundice), hung disorders, prostrate disorders (benign enlargement, nodular hyperplasia), colon disorders (action and dermal fibroblast disorders. Human 22406 cDNA is also useful in gene therapy ö Human; pyridoxal-phosphate dependent enzyme; 22406; acyltransferase; 32447; AfPase; 7716; aminotransferase; 25233; ring finger protein; 8035; 84242; aminopeptidase; 55304; metallopeptidase; 5299; anthopeptidase; 51999; metallopeptidase; 5299; ADP-ribosyltransferase; 21999; metallopeptidase; 52020; ADP-ribosyltransferase; 21999; metalloma associated antigen; 52020; heart failure; ischaemic heart disease; mycorafial inferction; viral hepatitis; cancer; intracerebral haemorrhage; brain abscess; viral hepatitis; cancer; intracerebral haemorrhage; brain abscess; viral hepaticus's disease; amyotrophic lateral sclerosis; inflammatory bowel disease; Crohn's disease; inflammatory bowel disease; Crohn's disease; Gaps cDNA encoding human pyridoxal-phosphate dependent enzyme, 22406. ö Sequence 1770 BP; 499 A; 379 C; 410 G; 482 T; 0 U; 0 Other; 80.0%; Score 16; DB 5; Length 1770; 100.0%; Pred. No. 4.5e+02; 0; Indels 100.0%; Pred. No. \*... ADD22938 standard; cDNA; 1770 BP Claim 1; Fig 1; 121pp; English. 1183 TTAATGGAGAGTGGCT 1198 5 TTAATGGAGAGTGGCT 20 15-JAN-2004 (first entry) 16; Conservative Best Local Similarity ADD22938; Query Match Matches RESULT 48 ADD22936 à 셤

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The present invention relates to the isolation of a novel human pyridoxal phosphate dependent enzyme family member (22406), a human argued enzyme family member (22406), a human aminotransferase (25233), human ring finger proteins (8035 and 84243), a human minotransferase (25233), human ring finger proteins (8035 and 84243), a human ADP-cribosyltransferase (21999), and a human melanoma associated antigen (52030). Also disclosed are the polynucleotide sequences encoding these novel human proteins. The polynucleotides and polypeptides of the present invention are useful for diagnosing and treating discrers, such as heart canner, and the standard discase, such as heart intracerebral haemorrhage, brain abscess, Alzheimer's disease, Pick disease, Pick disease, amyotrophic lateral seclerosis, inflammatory bowel disease, Crohn's disease, benign prostatic hypertrophy and systemic lupus erythematosus. The present sequence encodes a human protein of the invention.
                                                                                                                                                                                                                                                                                                              New isolated 22406 nucleic acids and polypeptides, useful for diagnosing and treating 22406-mediated disorders, such as myocardial infarction, hypertension, atherosclerosis, viral hepatitis, cancer and/or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1770 BP; 499 A; 379 C; 410 G; 482 T; 0 U; 0 Other;
                                                                                                                                                                                                               Bandaru R, Glucksmann MA, Meyers RE, Rudolph-Owen LA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 1; 349pp; English.
28-DEC-2000; 2000US-0258517P.
20-FEB-2001; 2001US-00789300.
22-JUN-2001; 2001US-00887399.
18-JUL-2001; 2001US-00908928.
28-NOV-2001; 2001US-00996194.
27-DEC-2001; 2001US-0034864.
                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                          WPI; 2003-625445/59
                                                                                                                                                                                                                                                                                   P-PSDB; ADD22939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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; 0 80.0%; Score 16; DB 10; Length 1770; 100.0%; Pred. No. 4.5e+02; 0; Indels 100.0%; Preq. ... 5 TTAATGGAGAGTGGCT 20 Local Similarity 100. nes 16; Conservative Matches 슝

. 0

Gaps

TTAATGGAGAGTGGCT 1198 1183 g

AAH16282 standard; cDNA; 2477 AAH16282; RESULT 49 AAH16282 

Human cDNA sequence SEQ ID NO:15148. (first entry) 26-JUN-2001

Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

Homo sapiens. EP1074617-A2.

07-FEB-2001

28-JUL-2000; 2000EP-00116126

29-JUL-1999; 99JP-00248036. 27-AUG-1999; 99JP-00300253. 11-JAN-2000; 2000JP-00118776.

02-MAY-2000; 2000JP-00183767 09-JUN-2000; 2000JP-00241899

(HELI-) HELIX RES INST

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J; Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

WPI; 2001-318749/34.

Primer sets for synthesizing polymucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 8; SEQ ID NO 15148; 2537pp + Sequence Listing; English.

The present invention describes primer sets for synthesising 5602 full
(a) an oligo-dT primer and an oligonucleotide complementary to the

complementary strand of a polynucleotide which comprises one of the 5602

(c) complementary strand of a polynucleotide which comprises one of the 5602

(c) complementary strand of a polynucleotide which comprises a combination

(c) oligonucleotide comprises at least 15 nucleotides; or (b) a combination

(c) f an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

(c) f an oligonucleotide comprising a sequence complementary to the

complementary strand of a polynucleotide which comprises a 5'-end

c) sequence and an oligonucleotide comprising a sequence complementary to a

polynucleotide which comprises a 1'-end sequence, where the

c) ligonucleotide comprises at least 15 nucleotides and the combination of

c) ligonucleotide opprises at least 15 nucleotides and the compination of

c) ligonucleotide opprises at least 15 nucleotides and the compination of

c) particularly full-length comprises of the primers are also useful for the

c) particularly full-length obnAs. The primers are also useful for the

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c) che full-length companies of the primers are also useful for the

c) change asily without any specialised methods. AAH0146 to AAH0363

c) c) consonal disconding are used in the exemplification of the

c) consonal disconding are used in the exemplification of the present invention 

Sequence 2477 BP; 738 A; 535 C; 524 G; 680 T; 0 U; 0 Other;

Gaps ö 80.0%; Score 16; DB 4; Length 2477; 100.0%; Pred. No. 4.7e+02; ive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 16; Conservative

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20 5 TTAATGGAGAGTGGCT

g ਨੇ

RESULT 50

Human modifier of p21 (MP21) gene sequence SeqID48.

p21 pathway modulating agent; assay system; MP21; cytostatic; MP21 procein activity modulator; cancer; genetically modified animal; human; gene; ds.

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10-JUL-2002; 2002US-0394795P.
07-AUG-2002; 2002US-0401739P.
16-SEP-2002; 2002US-041010P.
30-DEC-2002; 2002US-0437158P.
                    (EXEL-) EXELIXIS INC.
                                       WPI; 2004-091358/09.
P-PSDB; ADI82543.
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Francis-Lang H, Friedman L, Kidd T, Roche S, Joo DM, Lickteig K; Amundsen CD, Hai B, Zhang H, Adamkewicz JI, Hammonds GR;

Identifying a candidate p21 pathway modulating agent, useful for treating a disease such as cancer, comprises contacting an assay system comprising a MP21 polypeptide or nucleic acid with a test agent.

Example 2; SEQ ID NO 48; 392pp; English.

This invention relates to a novel candidate p21 pathway modulating agent by contacting an assay system comprising an MP21 (modifier of p21) to polypeptide or nucleic acid with a test agent, where in the absence of the test agent the system provides a reference activity and detecting a test agent-biased activity of the assay system. The invention may be useful for the production of compounds with a cytostatic activity through modulation of MP21 protein activity. The MP21 polypeptide or nucleic acid can be used for identifying MP21 modulating agents useful as therapeutic targets for diagnosing cancer or treating disorders associated with a respective or impaired p21 and/or MP21 function. MP21 modulating agents are useful in diagnosis, therapy, for example treating cancer, and pharmaceutical development. The genetically modified animals may be used for in vivo assays to test for activity of a candidate p21 modulating agent, or to further assess the role of MP21 in a p21 pathway process. The present sequence is that of a human M21 gene which is an orthologue of a prosophila p21 modifier and which was used in the exemplification of the invention.

Sequence 2477 BP; 738 A; 535 C; 524 G; 680 T; 0 U; 0 Other;

; 0 Score 16; DB 12; Length 2477; Pred. No. 4.7e+02; 0; Mismatches 0; Indels 0 Match 80.0%; Scc Local Similarity 100.0%; Pr es 16; Conservative 0; Query Match Best Local S: Matches 16

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Gaps

5 TTAATGGAGAGTGGCT 20

1183 TTAATGGAGAGTGGCT 1198

Search completed: December 3, 2004, 02:25:23 Job time : 317.789 secs

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

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Minimum DB seq Maximum DB seq

Database

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AC166235 Rattus no
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AC167800 Homo Sapi
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BV017711 S212P6029 E63790 Novel adeno AY496030 Phalaenop AX370148 Phalaenop BX93564 Gallus ga AB162773 Human ade CQ715635 Sequence AR096541 Sequence AR140077 Sequence AR152942 Arabidops AR38774 Sequence AR38774 Sequence	AF199485 Dr.Sophil AV496015 Phalacanop AV072119 Aubidops AV072119 Aubidops AV073119 Aubidops AV08481 Drosophil BC024489 Mus muscu AF04489 Mus muscu BC024711 Mus muscu BC021313 Homo sapi BC013711 Mus muscu AV08172 Drosophil AV3880 Starfish (A AK05517 Candida c BC075351 Renopus t BC075351 Renopus t BC075351 Homo sapi BC075351 Homo sapi BC075351 Homo sapi BC025277 Homo sapi BC025277 Homo sapi BC025277 Homo sapi AF33873 Sequence BC014949 Homo sapi AF216963 Mus muscu AK431997 Homo sapi AF216961 Mus muscu AK41898 Sequence BC014949 Homo sapi AK07555 Kenopus 1 AK07589 G.gallus RN BC072416 Homo sapi AK17589 G.gallus RN BC07378 Sequence BC07478 Rattus sp. AK1089 Sequence AK096549 Sequence AK1089 Sequence AK57810 Sequence AK57810 Sequence AK57811 Sequence	AF414088 HOMO SADI AL136624 HOMO SADI AK172917 Mus muscu
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Sycamors in Direct Submission

Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CENO 18A, UK. E-mail enquirties: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jul 19, 2001 this sequence version replaced gi:14715342.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences unit only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMB, Sw., SWISSPROT; Tr., TREMBL; Wp., WORWPEP; Information on the WORMPEP database can be found a tt., Armington whis seminered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPII-3011 is from the library RPCI-11.1 constructed by the group of bieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Human DNA sequence from clone RPI1-3411 on chromosome 9, complete
sequence.
                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       Slaugenhaupt, S. and Gusella, J.F.
Gene for identifying individuals with familial dysautonomia
Patent: WO 02059381-A 1 01-AUG-2002;
The General Hospital Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 6; Length 66479;
Pred. No. 8.9;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Sequence 1 from Patent WO02059381.
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AL359692.9 GI:14970800
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
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Homo sapiens
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AUTHORS
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Detection of mutations in a gene encoding lkappab
kinase-complex-associated protein to diagnose familial dysautonomia
Patent: BP 1252532-A 8 24-UUL-2002;
Rubin, Berish Y. (US) Anderson, Silvia L. (US)
Location/Qualifiers
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AL1611661 Homo sapi
AC016140 Homo sapi
AF207550 Homo sapi
AC095066 Homo sapi
AL0342802 Human Chr
AL034407 Human DNA
AL805934 Human DNA
AL360229 Human DNA
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AC101094 Mus muscu
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AL69758 Human DNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 8 from Patent EP1225232.
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Best Local Similarity 100.
Matches 20; Conservative
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TITLE
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37241. 37362
note="Charlie4 repeat: matches 1823. .1956 of consensus"
37669. .37895
                                                                                     consensus"
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70ce="HELB repeat: matches 265. .364 of consensus"

21813. .21845

7note="Alu repeat: matches 3. .35 of consensus"

21876. .22184

7note="Aluga repeat: matches 1. .311 of consensus"

22578. .22715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 74. .210 of consensus" 22693. .22848 note="L2 repeat: matches 2572. .2745 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="122 repeat: matches 2116. .2353 of consensus"
33415. .33568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2605. .2695 of consensus"
8474. .25775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28807. .29114
/note="AluSg1 repeat: matches 1. .305 of consensus"
29115. .29296
/note="L2 repeat: matches 1963. .2157 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2496 of consensus"
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                        .7614. .17738
'note="MER5B repeat: matches 54. .174 of consensus"
                                                                                                                                                                                                                                                                                              note="THEIA repeat: matches 1. .353 of consensus"
9860. .21021
note="THEIA-internal repeat: matches 427. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                     Inte="AluSg repeat: matches 1. .302 of consensus" 21315. .21711 /note="THEIA-internal repeat: matches 29. .427 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29748. .30050
/note="AluSg repeat: matches 1. .303 of consensus"
80475. .30548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MLT1D repeat: matches 16. .505 of consensus"
                                                                                                                           note="AluJo repeat: matches 1. .292 of consensus"
8530. .19071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSx repeat: matches 1. .301 of consensus" (6871. .27694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NluSg repeat: matches 1. .310 of consensus"
39947
                                                                                                                                                                                                           repeat: matches 1. .313 of consensus"
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  .206 of consensus'
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// note="MIR repeat: matches 71. .137 of consensus"

25259. .25338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .183 of consensus"
                                                                                                                             repeat: matches 5748. .6223 of
                                                                                                                                                                                                                                  9441. 19472
"note="16 copies 2 mer tt 84% conserved"
9498. 19859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2157.
8807. .29114
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  note="MIR repeat: matches 100.
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40006. 40255
/note="match: STS: Em:G14836"
404777. 40798
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8479. .28806
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/note="CpG island"
                                                              .7769. .18234
'note="L1MD1 r
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21022. .21
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VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone RP11-3111 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RP11-3111 is at 1 in this sequence. The true left end of clone RP11-115J22 is at 76377 in this sequence. The true right end of clone RP11-139N8 is at 76382 in this
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note="Alusg repeat: matches 1. .297 of consensus" 3074. .1357
                                                                                                                                                                                                                                                                                                                                                                 note="L1PB1 repeat: matches 5343. .6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191. .3349
note="AluSg/x repeat: matches 153. .311 of consensus"
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note="L1MC4 repeat: matches 6481. .6679 of consensus"
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note="AluSg/x repeat: matches 178. .295 of consensus"
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note="MBRSB repeat: matches 54. .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                        91. .1328
note="MER46B repeat: matches 3. .231 of consensus"
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note="AluSx repeat: matches 1. .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314. .5579
note="AluJb repeat: matches 1. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              881. .6013
note="AluJb repeat: matches 1. .135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849. .10232
note="MER84 repeat: matches 3. .373 of consensus"
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3411. .13533
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17189. .17296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="18 copies 2 mer tt 86% conserved"
                                                                                                                                                                                                                  'organism="Homo sapiens'
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/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                       clone lib="RPCI-11.1" 7. .829
                                                                                                                                                                   Location/Qualifiers
1. .78376
                                                                                                                                                                                                                                                                                                     'clone="RP11-3J11"
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note="MSTA re
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/note="MIR r
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(Theses I to 137930)

Nation. H., Alsbrooks.S., Amin,A., Anguiano,D.,
Anjan,H., Alsbrooks.S., Amin,A., Anguiano,D.,
Anjan,H., Alsbrooks.S., Amin,A., Anguiano,D.,
Anjan,H., Alsbrooks.S., Amin,A., Anguiano,D.,
Anjan,D., Bandarranike,D., Barber,M., Barner, Bacan,H., Benahmed,F.,
Biswalo,X., Blair,J., Blarkenburg,K., Blyth,P., Eaccan,H.,
Cardenas,V., Carter,K., Cavazo,I., Calderon,E.,
Chacko,J., Chavez,D., Chan,G., Chon,R., Chen,Y., Chen,Z.,
Claveland,C., Cocktel,R., Cox,C., Coyle,M., Care,A., D'Souza,L.,
Davila,M.L., Davis,C., Deramo,C., Ding,Y., Duval,B., Baves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Frandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Gebree,P.,
Frandez,S., Finley,M., Andra,R., Garner,M., Guerz,M.,
Gebregeorgis,E., Falls,Y., Call,R., Garley,M., Guerz,M., Gebree,P., Havlak,P., Hume,J., Idlebird,D., Jolivet,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Johnson,R., Martinez,B., Martine
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***, 50 unordered pieces.
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/note="match: STS: Em:G21606"
41261. .41395
/note="LINE2 repeat: matches 6041, .6161 of consensus"
41739. .41805
/note="TIGGER2 repeat: matches 2653. .2718 of consensus"
41806. .42093
                                                                                                                                                 /note="AluJb repeat: matches 1. .300 of consensus" 42094. .43429 / hote=="TIGGER2 repeat: matches 1302. .2653 of consensus" 43429. .44232 / hote=="TIGGER2 repeat: matches 297. .1113 of consensus" 44353. .44664
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Sison, Sitter, C.D. Smajs, D., Shetty, J., Shvartsbeyn, A., Sister, C.D., Smajs, D., Snedargren, E., Socalle, R., Socalle, M., Strong, R., Sutton, A., Soatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trajes, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, T., Walker, B., Wang, J., Wang, S., Warren, T., Wooden, H., Warley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Yoon, L., Yoon, V., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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NOTE: This is a 'working draft' sequence. It currently consists of 50 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Workley, n.v.

Direct Submission

Submitted (27-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 11, 2003 this sequence version replaced gi:28894576.

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.

Direct Submission

Submitsed (10-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases I to 137930)

Morley, K.C.
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f unknown length
g of 1836 bp in length
unknown length
g of 2917 bp in length
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of 1483 bp in length
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of 1720 bp in length
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           contig of 1673 b
gap of unknown 1
contig of 1549 b
gap of unknown 1
contig of 2256 b
gap of unknown 1
contig of 1367 b
contig of 1367
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Rattus.

12 (Dases 1 to 217073)

13 Millon H., Albbrooks S., Amin.A., Angulano.D.

14 Albbrooks S., Amin.A., Angulano.D.

15 Allan, C., Allan, H., Albbrooks S., Amin.A., Angulano.D.

16 Allan, C., Allan, H., Albbrooks S., Amin.A., Angulano.D.

17 Allan, D., Albarooks S., Amin.A., Angulano.D.

18 Baddin, D., Bandaranaiks, Barber, W., Barnetedd, M., Benahmed, F., Blandan, D., Blandaranaiks, C., Cadecon. E.,

18 Brawalo, K., Blant, C., Barber, C., Cadecon. E.,

18 Cardenas, V., Cartez, C., Cavas, T., Casar, H., Center, A.,

18 Cardenas, V., Cartez, C., Cavas, T., Casar, H., Center, A.,

19 Cardenas, V., Cartez, C., Cavas, T., Casar, M., Cree, A., D'Scouza, L.,

10 Cardenas, V., Cartez, C., Coyle, M., Cree, A., D'Scouza, L.,

10 Davis, C., Cockell, R., Cox, C., Coyle, M., Cree, A., D'Scouza, L.,

10 Dajddo, O., Denson, S., Denson, C., Ding, Y., Dinh, H., Dinya, K.,

10 Dajddo, O., Denson, S., Denson, C., Ding, Y., Dinh, H., Dinya, K.,

10 Dagper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Diva, R.,

10 Esenaide, S., Fallay, M., Flaggy, N., Forbes, L., Foster, M.,

11 Gabrageorgis, E., Geer, K., Gill, R., Cartia, M., Garria, M.,

12 Gebregeorgis, E., Geer, K., Gill, R., Cardia, M., Garria, M.,

13 Gackson, L., Hadal, S., Hadal, S., Hamilton, C., Hamilton, C., Hamilton, K.,

14 Harnarde, R., Haladu, S., Hune, J., Idlebird, D., Jackbird, D.,

15 Jan, M., Liu, Y., Lebow, H., Levan, J., Lows, L., Liu, X., Ma, J.,

16 Jan, M., Liu, Y., Lebow, H., Levan, J., Lows, S., Man, Z., Liu, X., Ma, J.,

16 Jan, M., Man, Liu, Y., London, P., Longare, S., Lopes, J.,

16 Jan, J., Liu, M., Mantin, K., Martin, R., Malloy, M., Malloy, M., Malloy, M.,

17 Jan, M., Man, M., Malloy, M., Malloy, M., Malloy, M., Malloy, M.,

18 Jan, Mapua, P., Mattin, K., Martin, R., Malloy, M., Malloy, M., Malloy, M.,

18 Mangum, B., Mapua, P., Mattin, K., Martin, R., Mangum, A., Mangum, A., Mandud, M., Mallos, M., Mallos, M., Mallos, M., Mallos, M., Repers, M., Palas, S., Reves, K., Palas, F., Rodorgen, M., Polinder, M., Norris, S., Marten, M., Reves, R., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC114144 217073 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-141D21, *** SEQUENCING IN PROGRESS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                   DB 2; Length 137930;
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0
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113922: contig of 5549 bp in length
114022: gap of unknown length
121300: contig of 7278 bp in length
121400: gap of unknown length
1248013: contig of 6813 bp in length
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HTG; HTGS_PHASEZ; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Pred. No. 67;
0; Mismatches
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                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 13, 2003 this sequence version replaced gi:23110872.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bom.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 217073: contig of 217073 bp in length.
                                                                                                                                                                                                                    Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, Y., Zhou, X., Zhao, S., Dunn, D., Yoo, V., Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinscock, G. and Gibbs, R.A.
Unpublished
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                                                                                                                                                                                                                                                                                                                    (bases 1 to 217073)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                          2 (bases 1 to 217073)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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JOURNAL
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AUTHORS
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JOURNAL
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92.0%; Score 18.4; DB 2; Length 217073;

Query Match

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ALE URDUBLISHED

URDUBLISHED

EVERTHER, L. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastlen, V., Boguslavky, L., Boukhgalter, B., Berren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Double, S., Barra, S., Bastlen, V., Boguslavky, L., Boukhgalter, B., Brown, A., Camarata, N., Camarata, J., Callans, S., Collymore, A., Cook, A., Cooke, P., Collins, S., Collymore, A., Cooke, A., Cooke, P., Cooke, P., Cooke, P., Cooke, A., Cooke, M., Gage, D., Galagan, J., Gardare, S., Ginde, S., Kalas, A., Kalle, M., Grahm, L., Grand-Fierre, N., Gord, J., Levine, R., Littev, T., Ohnson, R., Jones, C., McCarthy, M., McKerran, K., Relis, C., Lakooque, L., Mikova, T., Manat, P., Wickerran, K., Relis, C., Lakooque, L., Mikova, T., Manat, P., Wickerran, K., Patter, J., Warthews, C., McCarthy, M., Murphy, T., Navlor, J., Wenthy, P., Connor, T., O'Donno, L., Willey, R., Leis, C., Rogov, P., Roman, J., Reback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Reback, M., Riley, R., Rise, C., Rogov, P., Roman, S., Strauss, M., Tavaks, M., Travis, M., Trigillo, J., Vasaillev, H., Vashon, J., Zambek, L., Zimmer, A., and Zody, M. Dollara, V., Roman, S., Subraminssion

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                                                                                                                                                                                                                                                                                                                  AC110250 219359 bp DNA linear ROD 01-APR-2004
Mus musculus chromosome 1, clone RP23-260K6, complete sequence.
AC110250
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 219359)
                                          Gaps
                                          ..
                                          Indels
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Mus musculus chromosome 1, clone RP23-260K6
                                          ä
                                          Mismatches
       67;
       Pred. No.
                                                                                                                                                                    39797 GCAGTTAATTGAGAGTGGCT 39816
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Mus musculus
                                                                                                       1 GCAGTTAATGGAGAGTGGCT 20
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95.0%;
                                          19; Conservative
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Indels
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92.0%; Score 18.4; DB 10;
Best Local Similarity 95.0%; Pred. No. 67;
Matches 19; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                        / Prof. femily="Lx8" | 8095. . 8129 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 | 7.00 |
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloowin, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloowin, M., Diaz, J.S., Cook, A., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Erickson, J., Paro, S., Ferreira, P., PittGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T. Levine, R., Lindblad-Toh, R., Liu, G., Liu, K., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Mathews, C., McCarthy, M., Meldrim, J., Mencus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Betreson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Riee, C., Rogov, P., Roman, J., Schauer, S., Theodore, J., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Direct, Submission

All repeats were identified using Repeatmasker: html

Center: Whitehead Institute/MIT Center for Genome Research
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@broad.mit.edu
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Center clone name: 260_K_6
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94.7%;
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DIDPLANDDYGGSGGKYLKDFQNNKHRYLLASENQR PONFSTASMGSLTSSPSSCSLNS
GAGLTSVST SO DER INGTPGGAEAL IERKESEKI TABLINETREKLASKTERIRKEAL
LAEMGVATERDGYTGGYSPRKTPHLVNLNIDPLAGSCLLYY IKDGTTRVGQADAERR
QDIVLSGAHIKEEHCIFRSERNYTGEVIVTLEPCERSETYNGKRVAHPVQLRSGNRI
IMGKNHVFRENHBEGARAEREKTPSAEPVDWTFAQRELLEKQGIDMGOENBEKRL
QHEFELLAQMAFRKWRSEQPLIDLAGNAVLKGANATSYTEKEEBEEEEEVWT
CHEFELLAQMAFRKWRSHQFTSLANGLAGNAVLKGATTAYLTDTI
SPVPPELLAQMAFRKWRSHQFTSLANGLAGNAVLKGANATIYNSLLAGTT
VSPVPPELLAGNAFRKWRGTTVVAVUQDLKNGATHYWSLDKLKQRLDLMREMY
                                                                               AB070355 6032 bp mRNA linear ROD 02-APR-2002 Rattus norvegicus mRNA for kinesin-family protein 1Bp204, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MgGaSVKVAVRVRPFNSRETSKESKCIIOMOGNSTSIINPKNPK
EAPKSFSFDYSYWSHTSPEDPCFASQSRVYNDIGKEMLLHAFEGYNVCIFAYGOTGAG
KSYTWMGKQEESQAGIIPQLCEELFEKINDNCNEDMSYSVEVSYMEIYCERVRDLLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNKGNLRVREHPLLGPYVEDLSKLAVTSYTDI ADLMDAGNKARTVAATNMNETSSRSH
AVFTIVFTQKKQDPETNLSTEKVSKI SLVDLAGSERADSTGAKGTRLKEGANINKSLT
TLGKVI SALAEVDNCTSKSKKKKTDPI PYRDSVLTWLLRENLGGNSRTAMVAALSPA
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TADSDITELADEQQDAMEDFDDEAFVDDTGSDAGTEEGSELFSDGHDPFYDRSPWFIL
VGRAFVYLSNLLYPVPLIHRVAIVSEKGEVRGFLRVAVQAIAADEEAPDYGSGIRQSG
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KSGTLLDGKAVMEGFSEEIGNHLKLGSAFTFRVTVLQASGILPPYADIFCGFNFLHRH
DEAFSTEPLKNNGRGSPLGFYHVQNIAVEVTESFVDYIKTKPIVFEVFGHYQQHPLHL
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PTGEYIPAVVDHTAGLPCQGTFLLHQGIQRRITVTIIHEKGSELHWKDVRELVVGRIR
NKPEVDEAAVDAILSINIISAKSLKSSHSSRTFYRPBAVWDSSLHNSLLLNRVTPYG
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IIPTVETPYLARAGKNEFLNLVPDIEEVRAGSVVSKKGYLHFKEFLSSNWAKHFVVVR
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ELEKLELLHEVEKTRHFLLIRERLGDSIPKSMSDSLSPSLSSGTLSTSTSISSOISTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-AUG-2001) Norihiro Nakamura, Osaka University, Dept. of Biol., Grad. Sch. of Sci.; Machikaneyama, Toyonaka, Osaka 560-0032, Japan (E-mail:nnakamur@bio.sci.osaka·u.ac.jp, Iel:81-6-6850-5820, Rax.81-6-6850-5817)
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                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                               Miyake,Y., Nakamura,N., Matsushita,M., Tanaka,S., Inoue,H. and
Kanazawa,H.
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Kanazawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="kinesin-family protein 1Bp204"
/protein id="BAB86917.1"
/db_xref="GI:19911181"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rat kinesin-family protein, KIF1Bp204 isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue type="brain"
clone_lib="pGAD10 rat brain cDNA"
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organism="Rattus norvegicus"
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'db_xref="taxon:10116"
                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
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/gene="KIF1Bp204"
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Chases 1 to 53722)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Adderson, S., Barna, N., Bastien, V., Boquelavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cok, A., Charelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Garanc-Plerre, N., Hagos, B., Haford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Landers, T., Levine, R., Liu, G., MacChand, P., McKernan, T., Martuhe, R., Liu, G., MacChand, C., MacGonald, P., Major, J., Martuhe, R., Liu, G., MacGonald, P., Major, J., Devine, R., Mathova, T., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Petra, R., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rete, R., Spencer, B., Stanger, Theodore, J., Raymond, C., Retta, R., Rieback, M., Santos, R., Schauer, S., Schupback, R., Straus, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

All repeats were identified using Repeathmasker:

Research, 320 Charles Street, Cambridge, MA, 02141, USA

All repeats were identified using Repeathmasker:

Research, 200 Charles Street, Cambridge, MA, 02141, USA

All repeats were identified using Repeathmasker:

Research, 200 Charles Street, Cambridge, MA, 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                     ALLUU641 53722 bp DNA linear HTG 22-NOV-2001 Mus musculus clone RP23-162D22, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIOCATI. GI:17048007
HTG; HTGS PHASE0.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                            Gaps
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Length 6032;
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                   1, Indels
Score 17.4; DB 10;
Pred. No. 2.4e+02;
0; Mismatches 1;
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Center clone name: 162 D 22
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will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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Gaps ö Length 53722; 227 28926; gap of 100 bp brown length 360 31359; contig of 708 bp in length 460 3176; contig of 708 bp in length 360 31359; contig of 708 bp in length 177 32026; gap of 100 bp brown length 31021; contig of 745 bp in length 31021; contig of 745 bp in length 673 31972; gap of 100 bp brown length 31021; contig of 745 bp in length 31021; contig of 745 bp in length 670 31021; contig of 725 bp in length 670 3100; gap of 100 bp brown length 670 310; gap of 100 1; Indels of 734 bp in length Query Match

87.0%; Score 17.4; DB 2;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1; contig of gap of 100 contig of

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such one plasmid subclone or more than one Mil subclone, and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em.; EMBL; Sw.; SMISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/FGP/Chr!

RP4-796FB is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: POTABLE OF CHARLE OF CONSTRUCTED by the group of http://www.chori.org/bacpac/home.htm
                                                                                                                                                                         HS796F18 118968 bp DNA linear PRI 04-MAR-2003
Human DNA sequence from clone RP4-796F18 on chromosome
1956.11-36.33, complete sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (04-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. B-mail enquirises: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 23, 1999 this sequence version replaced gi:4455618.
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/db_xref="RZPD:RPCIP704F18796"
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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/clone="RP4-796F18"
/clone_lib="RPCI-4"
2188 GCAGTGAATGGAGAGTGGC 2170
                                                                                                                                                                                                                                                                                                        AL031291.3 GI:4481883
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ANATHOL. ANAISON. A. Ayodali. A. Andama. C., Addar. J., Andalah. A. Andali. M. Barnatead. M., Berdan. H., Beldan. H., Cavason. H., Carler, A., Chan. J., Chan. J., Chan. J., Chan. J., Charler, A., Charler, M., Creat. J., Chan. H., Charler, M., Creat. J., Chan. H., Charler, M., Creat. J., Chan. H., Daylan. H., Baran. H., Carler, M., Cabilan. H., Daylan. H., Baran. H., Carler, M., Cabilan. H., Daylan. H., Baran. H., Daylan. H., Baran. H., Daylan. H., Baran. H., Harlak. P., Hawel. H., Hanlah. H., Hanlak. P., Hamilton. K., Hamilton. H., Harlak. P., Hanlah. H., Haddan. S. L., Hanlah. H., Haddan. H., Haddan. S. L., Hanlah. H., Haddan. H., Ha
                                                                                                                                      | 153412 bp DNA linear HTG 19-NOV-2002 | Rattus norvegicus clone CH230-132J21, *** SEQUENCING IN PROGRESS | AC118949
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                  AC118949.7 GI:25073628
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
28369 CAGATAATGGAGAGTGGCT 28387
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Direct Submission
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AC118949/c
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HTG 11-SEP-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
     Homo sapiens chromosome 1 clone RP11-563B4, 21 unordered pieces. AL357135.4 G1:10186550 HTG; HTGS PHASE1; HTGS_CANCELLED. Homo sapiens (human)
                                                                                                                                                                                                                                                                                                          Frume, Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:10039951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 164394 bases at least Q40
Consensus quality: 168063 bases at least Q20
Insert size: 168847; aum.of-contigs
Ouality coverage: 19510; 2.8% error; agarose-fp
Quality coverage: 1950 in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 21 conties. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1: gap of 100 bp
1: contig of 2930 bp in length
1: gap of 100 bp
1: gap of 100 bp
1: gap of 100 bp
2: contig of 333 bp in length
2: gap of 100 bp
3: contig of 333 bp in length
3: gap of 100 bp
3: contig of 1333 bp in length
3: contig of 1333 bp in length
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2936: gap of 100 bp
10280: contig of 7344 bp in length
10380: gap of 100 bp
20606: contig of 10226 bp in length
20706: gap of 100 bp
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of 9785 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: humquery@sanger.ac.uk
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Web site: http://www.sanger.ac.uk
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ORGANISM
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                                                                                                           Direct Summission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23194726.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a caffold in the Atlas assembly (a 'contig-scaffold'). Within each contig scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* vOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: Phray, version 0,990329
Consensus quality: 13663 bases at least (04)
Consensus quality: 139024 bases at least (03)
Consensus quality: 140253 bases at least (20)
Estimated insert size: 139226; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 153412)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.halp@bcm.tmc.edu
Contact: hgsc.halp@bcm.tmc.edu
Center project Information
Center project name: GUIA
Center clone name: CH230-13221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....- Genome Center
Center: Baylor College of Medicine
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                                                                                                Direct Submission
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us-10-050-189a-8.rge

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     84680
95096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172869 bp DNA linear HTG 06-NOV-2002
Rattus norvegicus clone CH230-195G2, *** SEQUENCING IN PROGRESS
AC135550
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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87.0%; Score 17.4; DB 2;
Best Local Similarity 94.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 1;
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HTG; PHASE1.
Rattus norvegicus (Norway rat.)
Rattus norvegicus
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or 1059 bp in length
f unknown length
1 of 1403 bp in length
unknown length
of 1286 t
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NOTE: This is a 'working draft' sequence. It currently consists of 76 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                     Unpublished to 172869)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (06-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Center: Baylor College of Medicine

Center code: Baylor College of Medicine

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Contact: hgsc-help@bcm.tmc.edu
Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soca, J., Steinle, M., Strong, R., Sutton, A., Syatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vara, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Maczyk, R., Woden, H., Worley, K., Wight, R., Wu, J., Yakub, S., Yen, J., Yoon, J., Yon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, S., Zhang, J., Smith, H.O., Weinstock, G. and Gibbs, R.A. Bith, D.R., Direct Submission
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2455: contig of 1082 bp in length
2555: gap of unknown length
3844: contig of 1189 bp in length
3844: gap of unknown length
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5003: contig of 1159 bp in length
5103: gap of unknown length
6408: contig of 1205 bp in length
7722: gap of unknown length
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1722: gap of unknown length
1723: gap of unknown length
1827: contig of 1105 bp in length
1853: contig of 123 bp in length
11553: gap of unknown length
13089: gap of unknown length
13089: gap of unknown length
14499: gap of unknown length
15723: contig of 1224 bp in length
17322: gap of unknown length
17322: contig of 1250 bp in length
18582: gap of unknown length
18582: contig of 1250 bp in length
18682: gap of unknown length
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                  Query Match 87.0%; Score 17.4; DB 2; Length 172869; Best Local Similarity 94.7%; Pred. No. 2.46+02; Matches 18; Conservative 0; Mismatches 1; Indels 0;
89848: contig of 1843 bp in length
89948: gap of unknown length
91836: contig of 1888 bp in length
91936: gap of unknown length
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HTG: HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                 60256 GCAGTTAATGGACAGTGGC 60238
                                                                                                                                                                                                                                                                       1 GCAGTTAATGGAGAGTGGC 19
88006
89849
89949
91837
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
AC135710
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
CEYWORDS
SOUNCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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Submitted (10-MAY-2003) Human Gencence Sequencing Center, Department of Moderular and Human Genceics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA.

On May 10, 2003 this sequence version replaced gi:25012181.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold in the Atlas by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the entime to reduce and criented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                    Submitted (21-OCT-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 217844) Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu.F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niedezhausezn,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.0%; Score 17.4; DB 2; Length 217844; 94.7%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                 Unpublished
2 (bases 1 to 217844)
Rat Genome Sequencing Consortium.
Direct Submission
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Best Local Similarity
Matches 18; Conservat
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셤 8

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Rattus.

Rattus.

Rattus.

Rattus.

Rattus.

Ruzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Anyalebechi, W., Aoyaci, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

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Fraser, C.M., Gabis, A., Garcia, A., Garner, T., Garza, M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acizy361

252428 bp DNA linear HTG 20-NOW-2002
***, 10 unordered pieces.
Acizy361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.0%; Score 17.4; DB 2; Length 220270; 94.7%; Pred. No. 2.3e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC129361.5 GI:25138171
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.
Rattus norvegicus
Rattus norvegicus
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12424. .220270."
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                                                                                                                              1. .2442
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2543. .8436
/note="assembly_name:Contig12"
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db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GCAGTTAATGGAGAGTGGC 19
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Best Local Similarity 94.7
Matches 18; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AC129361
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                                                                                                                                                                                                              ACL33519 220270 bp DNA linear HTG 09-JUN-2004 Mus musculus chromosome 5 clone RP23-178N8, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Mus musculus clone
Unpublished
2. (bases 1 to 220270)
MCPDerson,J.D. and Waterston,R.H.
Direct Submission
Submitted (13-SEP-2002) Genome Sequencing Center, 4444 Forest Park
3. (bases 1 to 220270)
                                                                                                                                                                                                                                                                                                                                                                                 AC133519.2 GI:48475388
AC133519.2 GI:48475388
AUG HUGS-PRASE1, HTGS_DRAFT, HTGS_ACTIVEPIN.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house)
Musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-UT)-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
On Jun 9, 2004 this sequence version replaced gi:22830511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality; 218635 bases at least Q40
Consensus quality; 219029 bases at least Q20
Consensus quality; 219205 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119616 CAGTTACTGGAGAGTGGCT 119634
                  2 CAGTTAATGGAGAGTGGCT 20
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2543
8497
8597
27384
27484
41119
41219
123324
123324
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                     RESULT 14
AC133519/c
                                                                                                                                                                                                                                                                                       DEFINITION
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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TITLE
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Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23321944.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.ucid/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Parlernak,S., Paul,H., Perez,A., Perez,L., Pfannkon,C., Plopper,F., Poindexter,A., Perez,L., Pfannkon,C., Puoroz,M., Cuiroz,J., Rachlin,E., Reves,K., Regier,M.A., Reigh,R., Refilly,W., Ren Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Shen,H., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Sheats,V.J., Shvartsbeyn,A., Sisson,I., Siter,C.D., Smajs,D., Sneed,A., Scdergren,E., Sutton,A., Savetek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walter,B., Wang,C., Wallson,R., Wleren,R., Wei,X., While,F., Willsams,G., Wallson,R., Waldron,L., Walth,E., Walght,D., Waldhon,R., Waldron,L., Walght,D., Walght,R., Wull, Yakub,S., Yen,J., Yoon,U., Yoo,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederbausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Walnstock,G. and Gibbs,R.A.
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NOTE: This is a "working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (29-JUL-2002) Human Genome Sequencing Center, Department Submitted (29-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 252428)
Rat Genome Sequencing Consortium.
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18380: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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TITLE
JOURNAL
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TITLE
JOURNAL
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252630 bp DNA linear HTG 10-MAY-2003
***, 3 unordered pieces.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 252630)
Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 87.0%; Score 17.4; DB 2; Length 252428; Best Local Similarity 94.7%; Pred. No. 2.38+02; Matches 18; Conservative 0; Mismatches 1; Indels 0;
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): gap of unknown length
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l: contig of 6344 bp in length
l: contig of 2987 bp in length
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i: gap of unknown length
i: contig of 14408 bp in length
i: contig of 14408 bp in length
i: gap of unknown length
i: gap of unknown length
i: contig of 12573 bp in length
i: gap of unknown length
                                                                                                                                                                                                                                                                                           249483: gap of unknown length
252428: contig of 2945 bp in length.
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HTG; HTGS_PHASE1; HTGS_DRAPT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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7.hote="wgs_contig"
22161. .23454
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7.0046...28504
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40217. 141056
note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                        clone="CH230-132P14"
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28605. .29988
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04489. .106119
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106219:
247882:
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93446:
93546:
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73066:
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                                                                                58561:
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247983
249384
249484
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28505
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58662
73067
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AC097422/c
LOCUS
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KEYWORDS
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AUTHORS
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Ranyaleseth, N. Abyogi, D. Nochell, M. Broal, Baden, H. Randle, R. Block, D. Bandardie, D. Burborn, M. Bandardie, D. Burborn, M. Buld, M. Bandardie, D. Burrell, M. Calleron, E. Grades, M. Buld, M. Bullay, C. Burnh, P. Burrell, M. Calleron, E. Cardensa, V. Catter, M. Canter, M. Canter,
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TITLE
JOURNAL
REFERENCE
                    AUTHORS
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                                                                 AUTHORS
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                                                         REFERENCE
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COMMENT

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AC123476
Rattus norvegicus clone CH230-54E17, *** SEQUENCING IN PROGRESS
***, unordered pieces.
AC123476
AC123476.4 G1:25137780
HTG; HTGS PHASE1; HTGS DRAFT, HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Lordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length " (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a "working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* tis not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.0%; Score 17.4; DB 2; Length 252630; 94.7%; Pred. No. 2.3e+02; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 246059: contig of 246059 bp in length
246060 246159: gap of unknown length
246160 249026: contig of 2867 bp in length
249027 249126: gap of unknown length
249127 252630: contig of 3504 bp in length.
Location/Qualifiers
Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs_end_extension
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complement(8851..9686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end_sequence:BH317725"
210372. .210481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end_sequence:BH317726"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="clone_boundary
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site:EcoRI
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/note="clone_boundary
clone_end:Sp6
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Best Local Similarity 94.7%
''-rhes 18; Conservative
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AC123476/C
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misc_feature
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                                                   RATCHES.

RATCHES.

RATCHES.

RATCHES.

ANNUARY, D. MARIE... Methodox, S., Annih. A., Angulano, D., Anjen. C., Allen., Alebrooks, S., Annih. A., Angulano, D., Anyalebeehi, V., Aoyagi, M., Modeli, M., Barastead, M., Barantead, M., Brahar, S., Balar, J., Barastead, M., Barantead, B., Barden, M., Balar, V., Blair, J., Blair, J., Blair, J., Blarken, M., Barnstead, M., Brahamed, F., Bradwin, D., Bandron, D., Chang, J., Jang, J., Handth, S.L., Hodgeon, A., Hodgeon, J., Jang, H., Jang, H., Johnson, R., Johnson, R., Manda, J., Lubbw, H., Levan, J., Levan, J., Lavis, L., Li, Z., Liu, J., Liu, W., Liu, Y., Liu, W., Liu, Y., Liu, W., Liu, Y., Liu, W., Liu, Y., Liu, W., Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23267686. The sequence in this sesembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.bgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.

Direct Submission

Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 286008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 286008)
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REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Phrap, version 0.990329
Consensus quality: 256108 bases at least Q40
Consensus quality: 258933 bases at least Q30
Consensus quality: 258933 bases at least Q30
Consensus quality: 256918 bases at least Q30
Estimated insert size: 257935; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 1981. 
                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .242265)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .------Project Information
Center project name: GXQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CH230-54E17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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29850. .31150
fnote="wgs_contig"
complement[241566..242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence: BH347016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="clone_boundary
clone_end:T7_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1988. .3047
/note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="wgs_contig"
.8278. .20497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .452
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end\_sequence: BH347018"

LOCUS

RESULT 18 G86517/c

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Hayashizaki, Y., Hayatsu, N., Hiramcto, K., Hiracka, T., Horta, I. Iida, J., Iida, Y., Ishakawa, M., Itoh, M., Kagawa, I., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kadaya, I., Kawai, J., Kawai, J., Kawai, M., Kadai, M., Kadaya, M., Kadai, M., Kadaya, M., Kadai, M., Matsubara, K., Marata, M., Maukiki, R., Murata, M., Maukiki, R., Marakaya, R., Mikura, J., Mikura, Y., Makaki, M., Mamiki, T., Marikawa, R., Mikura, J., Mikura, M., Mamiki, R., Chneda, E., Ohno, W., Ohtsuki, K., Oaka, M., Sano, H., Sasaki, M., Satoh, K., Satoh, K., Satoh, K., Satoh, K., Shibata, K., Shibata, K., Shinagawa, A., Suzuki, K., Satoh, K., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Tagami, M., Yanada, H., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

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                                                                                                                                                                                                               The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kinchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kinchimoto, N., Yazaki, J., Libikawa, M., Yamada, H., Obda, H., Hotta, I., Kojima, K., Namiki, T., Poundation of Advancement of International Science Genome Sequencing & Analysis Group. Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Kawai, T., Kodama, T., Kawamata, M., Yoshimura, A., Mixra, J., Kawai, T., Koda, M., Watsubo, S., Niikura, J., Kawai, T., Carninci, P., Adachi, J., Aiawa, K., Arakawa, T., Pubuda, S., Kawai, J., Kanidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Konno, H., Mayazaki, A., Osato, N., Ota, Y., Yoshino, M., and Hayashizaki, Y., Collection, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (31-70M-2003) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Oapan (E-mail:sKikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rice.

VEL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Chaldy,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namki,T.,
Chneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
Fish Ganome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Science 301 (5631), 376-379 (2003)
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       KEYWORDS
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                                                                                                                                                                                                            REFERENCE
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AXI19449.1 GI:37989072
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                                                                                                                                                                                                                                                                                                                                                                                                                     G86517 578 bp DNA linear STS 06-SEP-2002 S209P6502PD2.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protocol: WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSC3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                  Gaps
                                       Query Match 87.0%; Score 17.4; DB 2; Length 286008; Best Local Similarity 94.7%; Pred. No. 2.38+02; Matches 18; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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Mismatches 0; Indels
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320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Eax: 6172580903
Email: Kersli@genome.wi.mit.edu
Primer A: None
STS size: 578
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85.0%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 4.1
Matches 17; Conservative 0; Mismatches
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1. .578
/organism="Mus musculus"
                                                                                                                                                                                                                                                          55471 CAGTTACTGGAGAGTGGCT 55453
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Mus musculus
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AK119449
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                      Ryu.R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratcry in Riken; Gachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Harao, A., Hashizume, W., Hayashida, K., Hayashi, N., Hiramoto, K., Hiramoto, K., Hiramoto, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kouda, M., Kishikawa Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Masuyama, T., Mumasaki, R., Ohno, M., Osato, N., Ota, Y., Sattoh, H., Sakai, C., Sakai, K., Ohno, M., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sattoh, H., Sakai, C., Sakai, K., Sattoh, H., Sano, H., Sasaki, D., Sato, K., Shibata, K., Sano, H., Taqawa, A., Thadami, P., Tagawa, A., Tadawa, A., Tadami, M., Tagawa, A., Tadawa, A., Tadami, M., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashiaraki, Y., Towaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashiaraki, Y., Towaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashiaraki, Y.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 53724)

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Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db_xref="taxon:39947"
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HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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220 28319: gap of 100 bp
29426: contig of 1107 bp in length
427 28526: gap of 100 bp
28526: gap of 100 bp
806 30905: gap of 100 bp
906 32571: contig of 166 bp in length
572 38921: contig of 122 bp in length
672 38922: contig of 122 bp in length
893 33992: gap of 100 bp
993 35731: contig of 123 bp in length
732 38012: contig of 1739 bp in length
683 38731: contig of 2181 bp in length
691 45790: gap of 100 bp
692 45590: contig of 7578 bp in length
693 53602: contig of 7578 bp in length
693 53602: contig of 7712 bp in length
663 53724: contig of 122 bp in length.
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      misc_feature
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FEATURES

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, SMISSROT; Tr:, TREMBL; Wp:, WORNPEP; Information on the WORMPEP database can be found at the their source databases:

Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; Mp:, WORNPEP; Information on the WORMPEP database can be found at his plane, inconsistency over the length of monouncleotide A/T runs and conserved TA repeats. Where the which it is found the longest good quality representation will be
                                                                                                                                                                                                                                                                                                                                                                                                              BX276188 177660 bp DNA linear VRT 28-APR-2004 Zebrafish DNA sequence from clone CH211-245A19, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson http://www.sanger.ac.uk/Projects/D rerio/fishmask.shtml CH211-245A19 is from a CHORI-211 BRC library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-APR-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
Zfish-helpssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 28, 2004 this sequence version replaced gi:46406525.

Center: Wellcome Center
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                  Gaps
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Score 17; DB 2; Length 53724; Pred. No. 3.9e+02; 0; Mismatches 0; Indels (
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/mol type="genomic DNA"
/db xref="texon:7955"
/clone="CH311-245419"
/clone_lib="CHORI-211"
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EX276188.11 GI:46848206
           Query Match

Best Local Similarity 100.0%; P:
Matches 17; Conservative 0;
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Danio rerio
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Vo.A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Direct Submission
Submitted (11-Aug-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON ANG 11, 2004 this sequence version replaced gi:49658801.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                              Center: Whitehead Institute/MIT Center for Genome Research Center code: WIBR
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Human DNA sequence from clone RP3-435D1 on chromosome Xq25,
complete sequence.
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                                                                                                                                                                                                   /map="7"
/clone="RP23-170D4"
/clone_lib="RPCI-23 Female Mouse BAC"
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85.0%; Score 17; DB 2; Li
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0;

    178061
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/chromosome="7"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 178061)

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                                   Length 177660;
                                                                 0; Indels
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HTG; HTGS PHASE1; HTGS FULLTOP; HTGS ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                 Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 7, clone RP23-170D4
                               Score 17; DB 5; Le
Pred. No. 3.9e+02;
0; Mismatches 0;
                     85.0%; SCC.
100.0%; Pre
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Matches 17; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Consensus quality: 195307 bases at least Q40
Consensus quality: 201602 bases at least Q40
Consensus quality: 201602 bases at least Q30
Consensus quality: 204197 bases at least Q30
Insert size: 182000; agarcse-fp
Insert size: 206457; sum-of-contigs
Quality coverage: 8.2 in Q20 bases; agarcse-fp
Quality cov.
* Working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truis of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                      1 (bases 1 to 208657)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a MAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SW:SSROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/FOPjects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromaper. Further information can be found at http://www.sanger.ac.uk/GOP/ChrX

RPS-435D1 is from the library RPCI.3 constructed by the group of Pieter de Jong, For further details see http://www.chori.org/bacpac/home.htm

VECTOR: DCCAPION.
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208657 bp DNA linear HTG 05-SEP-2000
SEQUENCE, 23 unordered pieces.
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            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184975)
                                                                                                                                      Direct Submission
Submitted (07-4002-2003) Wellcome Trust Sanger Institute, Hinxton, Submitted (07-4004-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirises:
humquery@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
on Aug 7, 2003 this sequence version replaced gi:3191972.
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/mol_type="genomic DNA"
/db_xref="RZPD:RPCIP704D01435"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute
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Contact: humquery@sanger.ac.uk
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HTG: HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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/clone_lib="RPCI-3"
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1. .144
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="X"
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Mus musculus (house mouse)

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

CE 1 (bases 1 to 226567)

Stou.L., Fu.Y. and Roe, B.A.

Mus musculus Chromosome 10 BAC Clone rp23-20217

AL Unpublished

CE 2 (bases 1 to 226567)

AL Unpublished

CE 2 (bases 1 to 226567)

CE 2 (bases 1 to 226567)

AL Unpublished

CE 2 (bases 1 to 226567)

AL Unpublished

CE 2 (bases 1 to 226567)

AL Submitsed (17-AUG-2001) Department of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

CE 3 (bases 1 to 226567)

AL Submitsed (17-EBP-2002) Department of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

CE 4 (bases 1 to 226567)

AL Submitted (17-EBP-2002) Department of Chemistry And Biochemistry,

The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA

CE 5 (bases 1 to 226567)

CE 6 (bases 1 to 226567)

CE 73019, USA

CE 750019, USA
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/note=="assembly_fragment"

205739. .208657_

/note=="assembly_fragment"
note="assembly_fragment"
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vector_side:right"
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AL Submitted (08-007-2002) Human Genome Sequencing Center, Department of Modecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Seq 14, 2002 this sequence version replaced gi:21908462. On Sep 14, 2002 this sequence version replaced gi:21908462. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecs/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Louleeged, H., Lozado, R.J., Lewis, L., Li, Z., Maruth, Marlinez, S., Mapua, P., Martin, R., Martinez, B., Mapua, P., Martin, R., Martinez, E., Morleod, M. P., McNeill, T. Z., Meenen, E., Mangum, A., Mandlay, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Mangum, A., Mandlay, M., Morris, S., Morris, S., Munidasa, M., Murphy, M., Nair, L., Naokeris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nakenen, E., Patter, M., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, J., Perez, L., Pfannkoch, C., Plopper, P., Polndexter, A., Popovic, D., Primus, E., Pul, L.-L., Pusc, M., Quiroz, J., Rechlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Robe, R., Riggs, F., Riggs, F., Rose, M., Savery, G., Scherer, S., Scott, G., Shateman, S., Shen, H., Shetty, J., Shvartsbey, R., Stefan, R., Savery, G., Scherer, S., Scott, G., Shateman, K., Suton, A., Sodergren, E., Song, X., Z., Soctelle, R., Storg, R., Wei, X., White, P., Williams, M., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usman, K., Williams, G., Waright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yon, Weinstock, G. and Gibbs, R., Smith, D.R., Holt, R., Smith, H., Frank, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             To (bases 1 to 232203)

Worley, K. C.

Morley, K. C.

Submitsed (base)

Submitted (base)

Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Rat Genome Sequencing Consortium.

Direct Submission
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Assembly program: Phrep; version 0.990329
Consensus quality: 206067 bases at least Q40
Consensus quality: 2.10828 bases at least Q30
Consensus quality: 2.12578 bases at least Q20
Estimated insert size: 2.28129; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/clone="xp32-2021"
/clone lib="RPOI - 23 Female (C57BL/6J) Mouse BAC Library"
/note="This is one of two clones in the same well from
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                                                                                                                                                                                                                 OK 73019, USA
7 (bases 1 to 226567)
7 (bases 2 to 226567)
Direct Submission
Submitted (14-NOV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Kattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                             Submitted (23-007-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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ON 73019, USA
ON Nov 14, 2002 this sequence version replaced gi:24211257.
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
Center code:UOKNOR
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1. .226567
                              6 (bases 1 to 226567)
Zhou,L., Fu,Y. and Roe,B.A.
Direct Submission
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Matches 17; Conservative
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AC127933/c
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Rattus norvegicus clone CH230-125L23, WORKING DRAFT SEQUENCE, 4
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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HTG: HTGS_PHASB1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus Norway rat)
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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0;
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/clone="CH230-180F1"
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Plugge, M. Sakeris, M. Sakeris, M. Sakeris, M. Schart, M. Schart, M. Sakeris, M. Markeris, M. Wall, M. Sakeris, M. Markeris, M. Wall, M. Sakeris, M. Markeris, M. Wall, M. Markeris, M. Markeris, M. Wall, M. Markeris, M. Ma
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Direct Submission
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alden, H., Adbbrookks, S., Amin, A., Anguiano, D., Anyalebechi, W., Adyadeji, A., Baca, B., Baden, H., Balandenburg, R., Blyth, P., Bromn, M., Benahmed, F., Baldwin, D., Bundaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenag, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacker, D., Carce, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Darg, C., Ding, Y., Chen, Y., Chen, Y., Chen, Y., Egan, A., Escotto, M., Eugene, C., Evans, C., Ding, Y., Dinh, H., Dirya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, X., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fransandez, S., Fahley, M., Flagg, N., Foltey, M., Gaerra, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Hernandez, S., Haeland, W., Hanil, C., Hamilton, C., Hamilton, C., Hawis, D., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Khan, Z., Hongon, R., Johnson, S., Martin, R., Mortenay, M., Mallosa, M., Markervis, C., Neal, D., Newton, N., Norris, S., Markin, R., Markervis, C., Neal, D., Newton, N., Norris, S., Markin, R., Warkervis, C., Neal, D., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Nake, M., Markervis, C., Markin, M., Mallosa, M., Markervis, C., Marker, M., Markervis, C., Marker, M., Marker, M., Marker, M.
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Rattus norvegicus clone CH230-246A22, WORKING DRAFT SEQUENCE.
AC111661
AC111661.4 GI:25007472
HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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as soon as it is available and the accession number will be preserved.
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100.0%; Pred. No. 3.9e+02;
.ive 0; Mismatches 0; Indels
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
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Marches 17; Conservative
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243933
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245381
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Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Eavlor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Entre Chamiston

Direct Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON Nov 15, 2002 this sequence version replaced gi:23603922.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described in the feature table below represents a scaffold, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puszc, M., Quiroz, J., Rachlin, E., Reeves, K., Reggler, M., A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sheck, J., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Taylor, T., Trhomas, N., Thomas, N., Thomas, S., Tingey, A., Trabor, P., Taylor, C., Valas, R., Vera, V., Villacana, D., Waldron, L., Walker, B., Wang, J., Wang, G., Wallson, W., Wleck, R., Wei, K., White, F., Willson, W., Williams, S., Warren, R., Wei, K., Wei, K., Won, L., Yoon, L., Yoon, L., Yon, V., Wright, D., Wright, D., Warsh, V., Yakub, S., Yen, J., Yoon, L., Yoon, V., Wainstock, G. and Gibbs, R.A. Smith, D.R., Holt, R.A., Smith, D.R., Place, Submission
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This of a "working draft' sequence. It currently

* consists of a contige daps between the contige

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced
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1 247649: contig of 247649 bp in length.

Location/Qualifiers
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Center: Baylor College of Medicine
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Worley, K.C.
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Rattus norvegicus clone CH230-3M21, WORKING DRAFT SEQUENCE, 3
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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clone_end:T7
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AL (Dages I to 26/852)

Worley, K.C.

Direct Submission

AL Submitted (09-7002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sa (bases I to 26/852)

My Direct Submission

AL Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 This sequence version replaced gi:24818314.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a caffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch.C.,
Plopper,F., Poindexer,A., Popovic,D., Primus,E., Pul.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,M., Ren,Y., Rener,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Snedry,G., Savartsbeyn,A., Sisson,I., Sitter,C.D., Samjs,D.,
Sned,A., Sodergren,E., Song X.-Z., Sortl,G., Shatsman,S., Shen,H.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,M., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Waltes,F.,
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Wright,D., Wright,R., Wulc,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Wright,D., Wight,R., Wulc,S., Smith,D., Von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Direct Submission
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 243899 bases at least Q40

Consensus quality: 246985 bases at least Q30

Consensus quality: 249301 bases at least Q20

Estimated insert size: 252851; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-3M21
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Center code: BCM
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Direct Submission
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JOURNAL
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AUTHORS
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JOURNAL
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AUTHORS
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Muzny, D. Marte, Metrer, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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Fraser, C.M., Gabisi, A., Ganta, R., Gardy, M., Guerra, W.,
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Rattus norvegicus clone CH230-239E4, WORKING DRAFT SEQUENCE, 5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1 265123: contig of 265123 bp in length
24 265233: gap of unknown length
25 266791: contig of 1466 bp in length
27 266791: gap of unknown length
28 267852: contig of 1061 bp in length
29 Location/Qualifiers
1. .267852
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HTG; HTGS PHASEI; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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VERSION

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Direct Submission

Submitted (125-MXY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sat Genome Sequencing Consortium.

Direct Submission

Submitted (13-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:22857158

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas and whole genome shocgun sequencing reads assembled using Atlas and whole genome shocgun sequencing reads assembled using Atlas assembly (a 'contig-seaffold'). Within each contig described in the feature table below represents a soaffold in the Atlas assembly (a 'contig-seaffold'). Within each contig-saaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Na to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shocgun sequence reads Soth end sequences and whole genome shocgun sequence reads Soth end sequence and whole genome shocgun sequence reads Soth end sequence and whole genome shocgun sequence reads. Both end sequences and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence reads. Both end sequence and whole genome shocgun sequence and whole genome shocgun sequence and solutions.
* NOTE: Estimated insert size may differ from sequence length (see (Seebank Graft data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Atlas 3.0;
Consensus quality: 229292 bases at least Q40
Consensus quality: 232004 bases at least Q30
Consensus quality: 233776 bases at least Q20
Estimated insert size: 239318; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor College of Medicine
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Center clone name: CH230-239E4
Center clone Summary Statistics
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source

FEATURES

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Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreirs, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Kanat, A., Karatas, A., Kalls, C., Landers, T., Levine, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Jones, C., McCarthy, M., Madord, D., Major, J., Manning, J., Matthews, C., McCarthy, M., Madord, D., Midor, J., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Rachupka, A., Ramasam, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasam, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schaback, R., Seeman, S., Severy, P., Smith, C., Spencer, B., Strage-Thomann, M., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiltev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wassiltev, H., Venkataraman, V. S., Viel, R., Vo, M., Wilson, B., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23017: contig of 23017 bp in length 23117: gap of 100 bp 53875: contig of 30758 bp in length 53875: gap of 100 bp 57492: contig of 3517 bp in length 57592: gap of 100 bp 77209: contig of 19617 bp in length 77309: gap of 100 bp 81981: contig of 4572 bp in length 81981: gap of 100 bp 8125097: contig of 43116 bp in length 125197: gap of 100 bp 125197: gap of 100 bp 125197: gap of 100 bp 164588: contig of 39761 bp in length 164588: contig of 39761 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 4316 bp in length gap of 100 bp contig of 39761 bp in length contig of 1500 bp contig of 1500 bp in length contig of 1600 bp contig of 41767 bp in length gap of 100 bp contig of 52969 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .274998
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/ clone="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L19139
Center clone name: 39_C_23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%; Score 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180062:
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274998:
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57493
77210
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81882
81982
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Campopiano, A., Chang, J., Chazaro, B., Choppel, Y., Campopiano, A., Chang, J., Chararo, B., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Glande, S., Gord, S., Goyette, M., Gage, D., Galagan, U., Gardyna, S., Glande, S., Gord, S., Goyette, M., Talama, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lamazares, R., Landers, T., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Major, J., Liu, G., MacLean, C., Macdonald, P., Major, J., Levine, R., Liu, G., MacLean, C., MacCanald, P., Major, J., Marquis, N., Mathews, C., MacCanald, P., Major, J., Lavine, R., Liu, G., MacLean, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Paters, N., Palara, V., Raymond, C., Retta, R., Rieback, M., Sherer, S., Schupback, R., Stener, S., Schupback, R., Stener, S., Schupback, R., Stener, S., Stoner, S., Willen, M., Tavis, N., Talamas, J., Tastaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 20-FEB-2004
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 274998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barna, N., Bastlen, V., Bloom, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85.0%; Score 17; DB 2; Length 270720; 100.0%; Pred. No. 3.9e+02; tive 0; Mismatches 0; Indels 0
1 263852: contig of 263852 bp in length 363952 aga of unknown length 165343: contig of 1291 bp in length 2244 265343: gap of unknown length 3344 267058: contig of 1715 bp in length 159 268587: contig of 1715 bp in length 159 268587: contig of 1429 bp in length 1588 268687: gap of unknown length 1688 270720: contig of 2033 bp in length 16021ion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC102634 274998 bp DNA linear Mus musculus chromosome 10 clone RP23-39C23 map 10, IN PROGRESS ***, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC102634.4 GI:42716204
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 10, clone RP23-39C23
                                                                                                                                                                                                                                                                                                     1. .270720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                         265344
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RESULT 31 AC102634 LOCUS DEFINITION

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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

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RATEURS.

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AND CORDOLA, ARI-OSMAD, F. A. All-OSMAD, F. BANKS, T.,
BADARIA, J. BENAICS.

BADARIA, BOWING, J. BIRGO, M., BIRGE, K., BIAKENDURG, K., BORNIH, D.,
BUNCK, J. BOWING, S., BIRGO, M., BIOWN, E., BROWIN, J.,
BURNAY, E., BORIGH, D., BIRGO, K., BIAKELL, D.,
BURNAY, C., BURTCH, P., BURTCH, K. L., BYTG, N. C.,
CLEVELANG, C., CONC., C., CHANGO, J., CHARGE, D.,
CHANG, C., CHEN, Z., CHOWGHLY, I., DEGRICH, D.,
DELANGE, K. R., DELAGG, C., DEN, A., CARVELL, D.,
DELANGE, K. R., DELAGG, C., DEN, A., CARVELL, D.,
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DELAGG, C., BARTIS, C., DAY, CARTOLL, DEGRICH, D.,
EARLIST, FERTIGUED D., FLAGG, T., DING, Y., DINDH, H.,
DOUTHWAIR C., Edgar D., Edgar D., Edwards, C.C., Elbaj, C., ESCCECO, M.,
FALIS, T., FERTIGUED D., FLAGG, T., DIOTEN, K., J.
BATTIS, C., HARTIS, K., HART, M., HALLE, S., HAMILTON, K.,
HARTISCO, HARTIS, K., HART, M., HALLE, S., HARNE, A., HARTHARGE, J.,
HARTISCO, HARTIS, K., HART, M., HOUGHE, S., HOUGH, S., HOUGH, S., HOWER, M., MALTISCO, L.
LI, J., LI, Z., LICHCATG, C., LIGH, S., HUMB, J., KOVAT, C.,
LI, J., LI, LI, LI, LI, LI, LI, LI, M., LOUISEGG, H.,
MADRSHWAT, M., MADIA, P., MATTIN, R., MATTING, R., MATCH, R., MADOR, P., MATCH, R., M
                                                                                                                                                                                                                                                                                         ACU98451 282383 bp DNA linear HTG 12-SEP-2002 Rattus norvegicus clone CH230-2G23, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
Submitted (23-OCT-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 282383)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalía; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                         Gaps
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Best Local Similarity 100.0%; Pred. No. 3.9e+02; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           AC098451
AC098451.7 GI:22795073
HTG; HTGS_PHASE1.
Rattus norvegicus (Norway rat)
                                                                                                                                  85254 GTTAATGGAGAGTGGCT 85270
                                                                                            4 GITAATGGAGAGTGGCT 20
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Worley, K.C.
Direct Submission
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Unpublished
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AC098451/c
                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bom.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "vorking draft' sequence. It currently

* consists of 126 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
Submitted (12-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 12, 2002 this sequence version replaced gi:21953456.

Center: Baylor Center
Center: Baylor College of Medicine
                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Contact: http://www.hgsc.bcm.tmc.edu/
Contact: project Information
Center project Information
Center clone name: CH230-2G23
Center clone name: CH230-2G23
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 177494 bases at least Q40
Consensus quality: 177494 bases at least Q20
Consensus quality: 179920 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1471: contig of 1471 bp in length 1571: gap of unknown length 3005: gap of unknown length 4039: contig of 1334 bp in length 4039: contig of 1034 bp in length 4139: gap of unknown length 5376: gap of unknown length 536: contig of 1020 bp in length 6496: gap of unknown length 7551: contig of 1025 bp in length 7551: contig of 1025 bp in length 7551: gap of unknown length 8955: contig of 1056 bp in length 8955: contig of 1056 bp in length 10081: contig of 1056 bp in length 10081: contig of 1056 bp in length 10081: contig of unknown length 1
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contig of 1279 bp in length
gap of unknown length
contig of 1294 bp in length
gap of unknown length
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                                                                                                                                                                            AC106235.4 GI:30579748
HTG, HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway_rat)
Rattus norvegicus
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CQ834336
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                     Direct Submission.

L. Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Maylor Plaza, Houston, TX 77030, USA.

On May 13, 2003 this sequence version replaced gi:23321404.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bem.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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1532 30936: contig of 1750 bp in length
1533 30936: contig of 1720 bp in length
1537 31036: gap of unknown length
1537 44009: contig of 1250 bp in length
1531 44109: gap of unknown length
15333 39330: contig of 29521 bp in length
15331 339430: gap of unknown length
1533 341322: gap of unknown length
1533 341322: gap of unknown length
1533 34227: contig of 1435 bp in length
1533 34227: gap of unknown length
1528 345077: contig of 1150 bp in length
1528 345077: contig of 1150 bp in length
1528 345077: contig of 1150 bp in length
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Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Rat Genome Sequencing Consortium.
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clone_end:Sp6"_
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13732. .14767
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clone end:Sp6
site:EcoRI
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KYLAPFLRAVELTRAMQILYKGTLAVLLYLLHDPPEFLCOYHYGFCDVVPPRGIQLN
LILSAFPRNWELTRAMQILYKGTLAVLLYLLHDPPEFLCOYHYGFCDVVPPRGIQLNK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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T cell activating gene
Patent: WO 2004058805-A 207 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
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/note="wgs_end_extension
clone_end:T7"
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clone end:T7
site:EcoRI
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complement[286270.
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10117. .44009
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94530. .98001
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Matches 17; Conservative
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Koga, H.
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BD127513
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PVTFLSDLRSNLQVSNEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMSTITHSA
MIDIRONLAYDLDTEGRYLFLNAIANOLRYPNSHTHYFSCTMLYLFAEANTEALQBQI
TRVLLERLI VARPHPWGLLITFIELIKNPAFKFWNHEFVHCAPEIEKLFQSVAQCCMG
OKQAQQVMEGTGGS
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/ DECETH_16="CAH05381"

/ Ab_xref="C1:5083876"

/ Cb_xref="C1:5083876"

/ Cb_xref="C1:5083876"

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PVTFLSDLRSNLQVSNEPGNRYNLQLINALVLYVGTQAIAHTRNKGSTPSMSTITHSA
HMDIFQNLAVDLDTEGRYLFLNAIANQLRYPNSHTHYFSCTMLYLFAEANTEAIQEQI
TRVLLERLIVNRPHPWGLLITFIELIKNPAFKFWNHEFVHCAPEIEKLFQSVAQCCMG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 90.0%; Pred. No. 5.2e+02;
Conservative 0; Mismatches 2; Indels 0
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84.0%; Score 16.8; DB 6;
Best Local Similarity 90.0%; Pred. No. 5.2e+02;
Matches 18; Conservative 0; Mismatches 2;
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T cell activating gene
Patent: Wo 200405805-A 209 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
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/note="unnamed protein product"
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CQ83438 GI:50833875
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Homo sapiens
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Best Local Similarity
Matches 18; Conserv
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CQ834338
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CQ783174
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Primer for synthesizing full-length cDNA and use thereof.
BD127513
BD127513.1 GI:23222458
UP S0020177575-A/2944.
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/db_xref="d1:4550310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHAIPPTLAMNPQAQALRSLLEVVULGRNSRDAITAALGGLLQKAVEGLLDATGGLEDEZ
LLEXPRECHLAUVLKALODGRAYGSPMCKQITRCLIEGRDEYKNVEAVELLIRNHLVN
MQYDLHLAQSMENGLNYNAVARAMQIVKILLVBERSVAHYTRADLEHTIETHARINA
HSRGAMPEGLEQLARVRSNYARAMIDRAHGGENFWHGISGISGASEYDDPGFERKAEY
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AQAEQQHNPRANNPTMRAKCYHNLDAFVRLIALLVGHSGGRATVTKXINLLNKYLGIV
VGVLLQDHDVRQSEFQOLPYHRIFINLLELNAPEHVLETINPGTLTAFCNTFHILRP
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PMQILYKGTLRVLAVLLHDFPEFLCDYHYGFCDVIPPNCIQLRNILISAFPRNYRLPD
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SEPGONRYDLLINALVLYVGTQAIAHIHNKGSTPSNKTITHSAHMDIFQNLAVDLDT
EGRYLFLNAIANQLRYPNSHTHYFSCTMLYLFAEANTEAIQBQITRVLLERLIVNRPH
PWGLLITFIELIKNPF"
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JP 2002017375-A/2944
22-JAN-2002
07-JUL-2000
JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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                                                                                                                                                                                                                                                                                                                 Primers for synthesizing full length cDNA clones and their use
Patent: BP 1396543-A 3144 10-MAR-2004;
Research Association for Biotechnology (JP)
Location/Qualifiers
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Primer for synthesizing full-length CDNA and use thereof
Patent: JP 2002017375-A 2944 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2944
PD 22-JAN-2002
PP 07-JUL-2000 JP 2000553172
PP 07-JUL-2000 JP 2000553172
PI TOSHIO OTA, TETSUO NISHIKAMA, TAKAO ISOGAI, KOJI HAYASHI, S
PI SHIII,
PI SHIII,
PI SHIII,
PI SHIII,
PI SHIII,
PI TETSUJI OTSUKI, HISASHI KOGA
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Pred. No. 5.2e+02;
0; Mismatches 2;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Local Similarity 90.0%;
nes 18; Conservative 0
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Homo sapiens
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873 GCAGTCAATGGAGAATGGCT 892

6 12:24:37 2004

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FEATURES

ORIGIN

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2878 bp DNA linear PAT 17-JUL-2003 Human nucleic acid sequence originating in ovarian myoma tissue. BD203717
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09-APR-1998 DE 198 17 557.4
THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
ANDRE ROSENTHAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CI2NIS/09, A61K38/00, A61K48/00, A61P15/00, A61P35/00, C07K14/82, C07K16/32, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/
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Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human nucleic acid sequences from ovarian tumour tissue
Patent: WO 9953040-A 67 21-OCT-1999;
SCHMIT ARMIN (DB); SPECHT THOMAS (DB); DAHL EDGAR (DE); HINZMANN
BERND (DB); ROSENTHAL ANDRE (DE); METAGEN GES FUER GENOMFORSCHUN
(DE); PILARSKY CHRISTIAN (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574,
C12N15/00,A61K37/02,C12N5/00
Human nucleic acid sequence originating in ovarian myoma
tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.0%; Score 16.8; DB 6; Length 2878; 90.0%; Pred. No. 5.2e+02; ive 0; Mismatches 2; Indels 0;
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Seguence 67 from Patent WO9953040,
AX014872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                               BD203717.1 GI:33013487
JP 2002511252-A/58.
Homo sapiens (human)
Homo sapiens
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VERSION
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JOURNAL
                                                             RESULT 39
BD203717
                                                                                                                                               ACCESSION
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KEYWORDS
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Dases 1 to 2637)

E 2 (bases 1 to 2637)

S Isogai, T. and Otsuki, T.

Direct Submission

Direct Submission

Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Genomics Laboratory; Direct Supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
                                           10,
PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai, T., Ota, T., Nishikawa, T., Hayashi, K., Otsuki, T.,
Sugiyama, T., Suzuki, Y., Nagai, K., Sugano, S., Ishii, S.,
Kawai-Hio, Y., Saito, K., Yamamoto, J., Waka, Mata, Nakamura, Y.,
Kojima, S., Nagahari, K., Masuho, Y., Ono, T., Okano, K., Yoshikawa, Y.,
Astenka, S., Sasaki, N., Hattori, A., Okumura, K., Iwayanagi, T. and
Ninomiya, K.
NEDO, human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                          2; Indels 0; Gaps
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84.0%; Score 16.8; DB 9; Length 2637;

Best Local Similarity 90.0%; Pred. No. 5.2e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens CDNA FLJ90644 fis, clone PLACE1064168.
AK075125.
AK075125.1 GI:22761010
Oligo capping; fis (full insert sequence).
Homo sapiens (human)
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/mol_type="mrNA"
/db_xref="taxon:9606"
/dbo="PLACE104168"
/tissue type="placenta"
/clone lib="placenta"
/note="cloning vector: pME188FL3"
                                                                                                                      (19). (2637). Location/Qualifiers
                                                                                                                                                                 1. .2637
/organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.08
Matches 18; Conservative
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LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 38 AK075125

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ORGANISM

REFERENCE

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

COMMENT

FEATURES

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18; Conservative
                                                                                                                                                                                                                                                                                                                                             sapiens
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SOURCE
ORGANISM
                                                                                                                                                                                                              DEFINITION
                                                                                                                                                     RESULT 42
HSM801007
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AUTHORS
TITLE
JOURNAL
          Matches
                                                                                                                                                                                                                                                       ACCESSION
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Lycopersicon esculentum aldehyde oxidase (AO1) gene, partial cds.
AF259793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 3560)
Inin.X. Okada.K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Direct Submission
Submitted (21-APR-2000) Plant Function Laboratory, The Institute of
Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 3560)
Min,X., Okada,X., Brockmann,B., Koshiba,T. and Kamiya,Y.
Molecular cloning and expression patterns of three putative
functional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
oxidase pseudogenes in tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MREROKKGNLVFAVNGERFELPSVDPSTTLLHFLRSETCYKSPK
GCGEGGGGGAVVLIGKYEPKFKWCHEPSASSCLTLLCSLUGCSITTSEGLGWTBDGF
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GNLCRCTGYRPIADACKTFAADIDIEDLGFNSFWKKGDSKEMKVSKLPPYXPTKNFST
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TQRYDHYVDLRHIPELSIIKRDQTGIEVGATVTISKFISVLKEESHINLGSYGKLVSQ
KLADHMEKIA"
                                                                                                                                                                                              Gaps
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                                                                                                                                            84.0%; Score 16.8; DB 6; Length 2878; 90.0%; Pred. No. 5.2e+02; ive 0; Mismatches 2; Indels 0;
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/gene="AO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(1187, .1334,2676, .>3560)
gene="AO1"
EC_number="1.2.3.1"
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/db_xref="G1:10764222"
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/db_xref="taxon:9606"
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Location/Qualifiers
1. .2878
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/mol_type="genomic DNA"
/cultivar="Moneymaker"
/db_xref="texon:4081"
/tissue_type="leaf"
<1187. .>3556
                                                                                                                                                                                                                                                                       193 GCAGTCAATGGAGAATGGCT 212
                                                                                                                                                                                                                               1 GCAGTTAATGGAGAGTGGCT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                       AF259793.1 GI:10764221
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                                                                                                                                                                                      18; Conservative
                                                                                                                                            Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                              RESULT 41
AF259793
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Length 3560;

Score 16.8; DB 8; Pred. No. 5.2e+02;

84.0%;

Query Match Best Local Similarity

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3572)

S Poustka, A., Klein, M., Mewes, H. W., Gassenhuber, J. and Wiemann, S. Direct Submission.

Submitted (15-SEP-1999) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;

Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de;

Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project.

This clone (DKFZp434N241) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubherweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.blochem.mpg.de/proj/CDNA/.

Location/Qualifiers

1. 1572
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LCTBKOVEL ESYRAQDSQOHNPAÄNFYNTRAKCYKNIDAPKYBL TALLVEKSGEATNYTV
KINLLNKVLGIVVGYLOKYGSBFQOLPYHR IF MILLLELMAPENTET TARGTL
TAFCNTFHILRPTKAPGFVYAWLELISHRIPIARMLAHTPQQKGWPMYAQLLIDLFKY
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LSAFPRNMRLPDPFTPNLKVDMLSEINIAPRILTNFTGVMPPQFKKDLDSYLKTRSPV
TFLSDLRSNLQVSNEPGNRYNLQLINALVLYVGTQAIAHIHNKGSTPSMSTITHSAHM
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VLLERLIVNRPHPWGLLI TFI ELIKNPAFKFWNHEFVHCAPEI EKLFQSVAQCCMGQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="DKFZp434N241"
/note="KIAA1007, strong similarity to S.cerevisiae cdc39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="testis"
/clone lib="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
  Gaps
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0
  Indels
7
0; Mismatches
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/db_xref="taxon:9606"
/clone="DKFZp434N241"
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<1. .3303
                                                                                      1223 GCAGTTAATGGAGAGAGGTT 1242
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1. .3572
                                               1 GCAGTTAATGGAGAGTGGCT 20
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AL117492.1 GI:5911979
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AF258812
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                                                                                                                                                                                                                                                                                                        4500 bp mRNA linear PLN 11-OCT-2000
Lycopersicon esculentum aldehyde oxidase (AO1) mRNA, complete cds.
AP258808.1 GI:10764213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Min,X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Direct Submission
Submitted (20-APR-2000) Plant Function Laboratory, The Institute of Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi, Saitama 3510198, Japan
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/Figure="Molybdenum cofactor-binding enzyme"
/rodon start=1
/product="aldehyde oxidase"
/protein id="Ad022605.1"
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/db xref="G1:1078XFEVRWEPFSASSCLTLLCSLNGCSITTSEGLONTRDGF
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NGCISKGRKQKLLSSSKQYVEFFTEYSPLTDVHPSISGGLLDGINDISDKEVSDN
LHGAFIYSTKRLAGYKGIQLEBNHLTDTTIITYKDIPPGGANTGAVTPFGSEPLFAED
LLRCADET HAVVADSQRADLAAPTLIETDTTVNDSALLTVEEAVEKSSFIQVPP
FQPEQIGDFYKGMABADQKILSAELRFGSEYHFYMETQTALAIPDENKUMYYTSSQC
PENSQSMIASCLGVPAHNIRVITRRLGGAFGGKFVKAMPVSTACALAAYKLRFPVRIY
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YPEFLKSESATNLDSSKYPWSPVSIKELWGLLNFNVTVNRGSFKLVVGNTGTGYYKE
TQRYDHYVDLRHIPELSIIKRDQTGIEVGATVTISKFISVLKBESHINLGSYGKLVSQ
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TWEELLSRPPLDSKTVLLSVCI PPKKDQSSHQTHSRFLFETYRAAPRPHGNALAYVNA
AFQADVSHCNNGVLINNI YLAFGAYGTKHATRAKKVEECLTGKMLSVHVI VEALKLVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptcophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamidas; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 4500)
Min, X., Okada, K., Brockmann, B., Koshiba, T. and Kamiya, Y.
Molecular cloning and expression patterns of three putative
Lunctional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
                                                                                                                                                         Gaps
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                                                                                                           84.0%; Score 16.8; DB 9; Length 3572; 90.0%; Pred. No. 5.2e+02; Live 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/mol_type="mRNA"
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/db_xref="taxon:4081"
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                                             /gene="DKFZp434N241"
                                                                                                                                                                                                                       1413 GCAGTCAATGGAGAATGGCT 1432
                                                                                                                                                                                                1 GCAGTTAATGGAGAGTGGCT 20
QAQQVMEGTGAS"
3562
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181. .4266
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                                                                                                     Query Match
Best Local Similarity 90.0%
Matches 18; Conservative
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AF258808
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VNRNSDMIMTGGRHPMKVTYSVGFKSSGKITALHLDILINAGITDDLSPIIPSYLMNT
KKYNWGAESPIQVCKTNLTSKTIPRGPGBVQGSYIABALVEHVABLLESTBUDSVRN
BNVHTFESLNLFYGNVVAERGEYTLPSINDKLAVSSFFGRSKYNIEQPNOKNTWKRGI
SRVPAPVNASQRPPTGKVSILQDGSIVVBVGGSVDVGOGLWTKVRQWTAYALGSIESSR
AEDLVEKVRVIQADTLSVVQGGLTAGSTTSESSCAAVKLCCDILVERLITALKKQLQEK
NVSVOMPTLIRQAQTOSINLAANSYYVPEFLRYTTGAAVSENEIDVLTGETTILQSD
INTDGGQSLNAAVDLGQVBGAFVQGIGFFKKEEYTNBDGLMVSNSTWTYKIPTIDTI
PONFWHILVNSGHHBORULSSKTSGEPPLFAASVHAATRAAIRAARBGLKRWDKLDE
SASEFYLDVPAILPVVKTQCGLDYAEKFVETLLAARSTCFK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 4517)
Min.X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Direct Submission
Submitted (20-APR-2000) Plant Function Laboratory, The Institute of Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi, Saitama 1510198, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF258812 4517 bp mRNA linear PLN 11-OCT-2000 Lycopersicon esculentum aldehyde oxidase (AO5) pseudogene, mRNA
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Lycopersicon esculentum
Eukaryota, Viridiplantea, Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantea, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
I (basea I to 4217)
Min,X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Molecular cloning and expression patterns of three putative
Eunctional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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/mol_type="mRNA"
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/db_xref="taxon:4081"
/dev_stage="3 week-old wilting seedling"
1. -4517
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AX329720
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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90.0%; Pred
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Best Local Similarity 90.0<sup>3</sup>
Matches 18; Conservative
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Direct Submission
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Min.X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Min.X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Submitted (20-APR-2000) Plant Function Laboratory, The Institute of Physical and Chemical Research (RIKEN), 2-1 Hirosawa, Wako-Shi,
Location/Qualifiers
                                                                                                                           Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases I to 4631)
Min,X., Okada,K., Brockmann,B., Koshiba,T. and Kamiya,Y.
Molecular cloning and expression patterns of three putative
functional aldehyde oxidase genes and isolation of two aldehyde
oxidase pseudogenes in tomato
Biochim. Biophys. Acta 1493 (3), 337-341 (2000)
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TYPEFIKSESTTNLDSLRYSWYTPVSIBDLGSLLNSNVTBNGASFKLVVGNTGTGYYK
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PETSTKALAGVKGIQLESNQLTDGVAAVITFKDIPIGGANIGATRFSDEFBLFADDLV
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FHSIHERIAGFHASQCGFCTPGMCMSFFSALVNADKGNKPDPPPGFSKLTSSEAEKAI
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SVDMPTLIRQAQMQSVHLAAHSYYVPESSSKNYLNFGAAVSEVEIDILTGETTILQSD
IIXDCGQSLNPAIDLGQIEGAFVQGIGFFMHEEYLTNEDGLMVSNSTWTYKIPTIDTI
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SVSEFYLDVPAILPVVKTQCGLDYVEKYLETLVAQKSNYTCINMDLK"
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Lycopersicon esculentum aldehyde oxidase (AO2) mRNA, complete cds.
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note="molybdenum cofactor-binding enzyme"
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[. .4631
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/mol_type="mRNA"
/cultivar="Moneymaker"
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                                    AF258809
AF258809.1 GI:10764215
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets.

Patent: WO 0194629-A 229 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
PAT 09-JAN-2002
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 (bases 1 to 4977)
1 Hedvat, C.V. and Irving, S.G.
The isolation and characterization of MINOR, a novel mitogen-inducible nuclear orphan receptor Mol. Endocrinol. 9 (12), 1692-1700 (1995)
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linear
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Pred. No. 5.1e+02;
0; Mismatches 2; Indels
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/organism="Homo sapiens"
/mol_type="mkna"
/db xref="taxon:9606"
/cell type="T-1ymophocyte"
/tissue_type="peripheral blood"
DNA
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gene="MINOR"
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/ LAINGREAD STRIKERE VENCHIRNIE FEETR FPEOY POKELHITACLEGGIIEKGI

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FPHILOEN I SYGOGEN EPPENGOST TIPGGIALAQAQAQAQOYDAKAPLAGOVSTWY

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NPEFRINGAVIABIY NIXVILISDSKAAAN FSDRSLIKNIGHMIGMITLAKNK PILHTDL

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DVKSLILLEAYVKGQGELLIYVV PFVAKVIESSIRSVV FRPPENFWTMAIMWYLAELHQEH
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="Gq1:3821743"
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell activating gene
Patent: WO 2004058805-A 213 15-JUL-2004;
Asahi Kasei Pharma Corporation (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ834342 512 bp DNA Sequence 213 from Patent WO2004058805. CQ834342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. :5122
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alfa transcript"
3545. .3550
/gene="NOR-1"
/note="alfa transcript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="alfa transcript"
2168. .2173
/gene="NOR-1"
note="alfa transcript"
codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2044. .5115
/gene="NOR-1"
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Best Local Similarity 90.0
Matches 18; Conservative
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KEYWORDS
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LOCUS
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                                                                                                                                                              /protein_id="aAB02581.1"
//brotein_id="AB02581.1"
//db xref="0T:924282"
//db xref="0T:924282"
//cb xref="0T:924281"
//cb xref="0T:92
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Sus scrofa mRNA for neuron-derived orphan receptor-1 alfa transcription factor.
AJ011767
AJ011767
G1:3821742
AJ011767
Gerived orphan receptor-1 alfa; NOR-1 gene; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cases-Langhoff,C., Castello,A., Martinez-Gonzalez,J. and Badimon,L. De-differentiated smooth muscle cells in atherosclerotic plaques express NOR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (08-0CT-1998) Castello A., Patologia Molecular y
Terapeutica, Instituto de Investigaciones Biomedicas, C.S.I.C.,
Jordi Girona, 18-26, Barcelona, 08034, SPAIN
Location/Qualifiers
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                                                                                               'codon start=1
product="mitogen induced nuclear orphan receptor"
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84.0%; Score 16.8; DB 9; Length 4977;
Best Local Similarity 90.0%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
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/organism="Sus scrofa"
/mol type="manna"
/db xref="taxon:9823"
/cell type="activated smooth muscle"
/tissue_lib="smooth muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112. .2043
/gene="NOR-1"
/function="transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEDLVSPPSIIDKLFLDTLPF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MINOR"
/note="8 A residues"
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4977
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112. .2043
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/gene="NOR-1"
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/gene="MINOR"
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Sus scrofa (pig)
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VERSION
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AUTHORS
TITLE
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Rlausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheder, C.F., Bhat, N. K.,
Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schedtz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.N.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 5137)
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Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A, 99 (26), 16899-16903 (2002)
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SOURCE
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REFERENCE AUTHORS

JOURNAL

TITLE

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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305

Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 22 Row: 1 Column: 12.
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VLAELHQEHDLKLNIKFEIEVLCKOLLADDINELKOKDRLKOLDEQLSAPKKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKQPBELPPITTTTSTTPATNITCTATVPPQPQYSYHDINVYSLÄGLAPHITLNPTI
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DKCITELEQHLHAIPPTLAMNPQAQALRSLLEVVVLSRNSRDAIAALGLLQKAVEGLL
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ELLIRNHLVNMQQYDLHLAQSMENGLNYMAVARAMOLVKILLVDERSVAHVTEADLFH
TIETLMRINAHSRGNAPEGLPQLMEVVRSNYEAMIDRAHGGFNFMMHSGISQASEYDD
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TEMCVEISYRAQAEQQHNPAANPTMIRAKCYHNLDAFVRLIALLVKHSGEATNTVTKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLLNKVLGIVVGVLLQDHDVRQSEFQQLPYHRIFIMLLLELNAPEHVLETINFQTLTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFPRIMRLPDPFTPNLKVDMLSEINIAPRILINFTGVMPPQFKKDLDSYLKTRSPVTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LERLIVNRPHPWGLLITFIELIKNPAFKFWNHEFVHCAPEIEKLFQSVAQCCMGQKQA
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Conteact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Vector: pCMV-SPORT6"
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misc\_feature

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Matches 18; Conservative 0; Mismatches 2; Indels 0;
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nucleic search, using sw model

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nucleic

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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 1000 summaries

Database

3694831 seqs, 2747406616 residues

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Title: Perfect score:

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Scoring table:

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Copyright (c) 1993 - 2004 Compugen Ltd.
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DB

Length

Query Match

Score

Result No.

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US-09-998-598-249 US-09-895-828-217 5 US-10-114-666-217 6 US-10-264-237-38 TIS-09-898-309	US-10-114-666-309	US-10-6/4-124A-2331/ US-09-895-828-394	US-10-114-688-394 US-10-674-124A-2199	US-09-864-761-3871	US-10-027-632-36029	US-10-027-632-294020	US-10-027-632-36029 US-10-027-632-294020	US-10-425-114-34242	US-09-833-790-34	US-10-424-599-1618 US-10-242-535A-36691	US-10-242-535A-41317	US-10-085-783A-36691	US-10-085-783A-41317	US-10-43/-963-31409 US-10-424-599-28596	US-09-864-761-1885	US-10-242-535A-40187	US-10-085-783A-40187	US-10-085-783A-26709	US-10-424-599-109115	US-10-425-115-64439	US-10-027-632-56831 HS-10-027-632-56831	US-09-974-300-6943	US-09-918-995-8923	US-09-895-828-199 TTS-09-818-895-30990	US-10-114-666-199	US-09-918-995-19745	US-09-770-961-743	US-10-085-783A-17512	US-10-425-115-77130	US-10-027-632-45251	US-10-027-632-45250	US-10-027-632-45251 US-10-424-599-94933	US-09-918-995-23898	US-10-029-386-10404	US-10-767-701-6782	US-10-066-543-1385	US-10-424-399-101243 US-10-027-632-67854	US-10-027-632-67854	US-10-027-632-295478	US-10-02/-832-2934/8 US-10-027-632-85520	US-10-027-632-315014	US-10-027-632-85520	US-10-027-632-315014	US-10-027-53-083	US-10-027-632-271874	US-10-144-649A-683	US-10-027-632-271873	US-IU-UZ/-63Z-Z/IS/4 US-09-854-133-682	US-10-144-649A-682	US-10-425-115-125066
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RESULT 2
US-10-041-856-1/C
US-10-041-856-1/C
Sequence 1, Application US/10041856
Publication No. US2002016929941
GENERAL INFORMATION:
APPLICANT: SLAUGENHAUPT, SURAN
TITLE OF INVENTION: GENE FOR IDENTIFYING INDIVIDUALS WITH FAMILIAL.
TITLE OF INVENTION: DYSAUTONOMIA
FILE REFERENCE: 1829-4004081
CURRENT APPLICATION NUMBER: US/10/041,856
CURRENT APPLICATION NUMBER: US/02-07-08
PRICE FILING DATE: 2002-07-08
PRICE FILING DATE: 2001-01-06
NUMBER OF SEQ ID NOS: 88
CONTRACT PRICE PARENTE NOS: 88
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| Sequence 514, Application US/10087192
| Publication No. US20020182586A1
| GENERAL INPORMATION:
| APPLICANT: Morris, David W. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR ITILE OF INVENTION: CANCER CURRENT FILING DATE: 2020-03-01
| PRIOR PELLING DATE: 2020-03-01
| PRIOR FILING DATE: 2000-12-22
| PRIOR PELLING DATE: 2000-12-22
| PRIOR PELLING DATE: 2000-12-22
| PRIOR FILING DATE: 2000-13-02
| NUMBER OF SEQ ID NOS: 2059
| SEQ ID NOS: 2059
| SEQ ID NOS: 1058
| LENGTH: 71183
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82.0%; Score 16.4; DB 13;
Best Local Similarity 94.4%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 1;
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US-09-796-692-299
US-09-796-692-299, Application US/09796692
; Publication No. US2020198362A1
; GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (1)...(74183)

OTHER INFORMATION: n = A,T,C or G
US-10-087-192-514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-041-856-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 66479
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US-10-060-1894-7
US-10-060-1894-7
Sequence 7, Application US/10050189A
Sequence 7, Application WS/10050189A
Sequence 7, Application WS-100501865A1
GENERAL INFORMATION:
APPLICANT: Anderson, Sylvia
APPLICANT: Anderson, Sylvia
APPLICANT: Anderson, Sylvia
TITLE OF INVENTION: Percetion of Mutations in a Gene Encoding IXB Kinase-Complex-Asso;
FILE REFERENCE: Rubin 201
TITLE OF INVENTION: Protein to Diagnose Familial Dysautonomia
FILE REFERENCE: Rubin 201
CURRENT APPLICATION WHOBER: US/10/050,189A
CURRENT FILING DATE: 2002-01-16
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 20
                                                                                                                                                                        Sequence 34839, A Sequence 24839, A Sequence 279033, Sequence 279033, A Sequence 27903, A Sequence 273720, A Sequence 170635, Sequence 170635, Sequence 170635, Sequence 170635, Sequence 173703, Sequence 189797, A Sequ
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100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels
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ORGANISM: Homo sapiens
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US-US-19-796-692-3607

Sequence 3607, Application US/09796692

Sequence 3607, Application US/09796692

Sequence 3607, Application US/09796692

Sequence 3607, Application US/09796692

SEQUENCE CONTINUED US/020209362A1

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE PEREZENCE: 2071-001-200

CURRENT APPLICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-05-20

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR PILING DATE: 2000-05-20

PRIOR APPLICATION NUMBER: 60/220,999

PRIOR APPLICATION NUMBER: 60/220,999
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Pred. No. 3.9e+02;
0; Mismatches 2;
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: PASSEZ FOR WINGOWS Version 3.0
SENGTH: 182
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LOCATION: (1)...(182)

CTHER INFORMATION: n = A,T,C or G

US-09-796-692-453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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US-09-796-692-3607
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| Sequence 453, Application US/09796692
| Publication No. US20020198362A1
| GENERAL INFORMATION:
| APPLICANT: Algate, Paul A.
| APPLICANT: Mannion, Jane
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
| TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
| FILE REFERENCE: 2077.001200
| CURRENT APPLICATION NUMBER: 05/09/796,692
| CURRENT APPLICATION NUMBER: 60/190,479
| PRIOR APPLICATION NUMBER: 60/190,479
| PRIOR FILING DATE: 2000-03-01
| PRIOR FILING DATE: 2000-03-07
| PRIOR FILING DATE: 2000-03-07
| PRIOR FILING DATE: 2000-04-27
| PRIOR FILING DATE: 2000-04-27
| PRIOR FILING DATE: 2000-04-27
| PRIOR APPLICATION NUMBER: 60/200,303
                                   APPLICANT: CAGAGE, PAUL A.

APPLICANT: ALGAGE, PAUL A.

APPLICANT: MAINTON, UNIVERSITORS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEAMADICOGICAL MALIGNANCIES
TILR SPERRANCE: 2007.011-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,346
PRIOR APPLICATION NUMBER: 60/200,346
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-24
PRIOR PILING DATE: 2000-06-34
PRIOR PI
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; OTHER INFORMATION: n = A,T,C or G
US-09-796-692-299
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                       Gaiger, Alexander
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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US-09-796-692-453
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APPLICANT: Adgret. Alexander
APPLICANT: Adgret. Alexander
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Marc
APPLICANT: Retere. Marc
APPLICANT: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Tempositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
CHRENT TILLS OF INVENTION: Hematological Malignancies
CHRENT APPLICANTON NUMBER: US10/040,862
CHRENT APPLICANTON NUMBER: US 60/190,479
PRIOR APPLICANTON NUMBER: US 60/190,479
PRIOR PLINKO DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLINKO DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-10
PRIOR PLINKO DATE: 2000-05-11
PRIOR PLINKO DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-14
PRIOR PLINKO DATE: 2000-05-14
PRIOR PRIOR PLINKO DATE: 2000-05-14
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                                                                                                                                                                                                                                                  Length 182;
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                                                                                     ; LOCATION: (1) ... (182)
; OTHER INFORMATION: n = A,T,C or G
US-10-040-862-299
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; OTHER INFORMATION: n = A,T,C or G
US-10-040-862-453
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                                                       NAME/KEY: misc feature
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            FEATURE:
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APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352005
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
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79.0%; Score 15.8; DB 9; Length 182;
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PRILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DAT
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3607
LENGTH: 182
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Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 AGCTGCAACAGTACAATG 118
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                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: (54)
OTHER INFORMATION: n=A,T,C or G
NAME/KEY: unsure
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; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-3607
                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                  TYPE: DNA
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APPLICANT: Magnaton, Jane
APPLICANT: Magnaton, Jane
APPLICANT: Manion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Cather, Jonathan David
APPLICANT: Cather Composition
APPLICANT: Corixa Corposation
APPLICANT: Corixa Corposation
APPLICANT: Modelli, Particia Dianne
APPLICANT: Modelli, Particia Dianne
APPLICANT: Corixa Corposation
APPLICANT: Modelli, Particia Dianne
APPLICANT: Modelli, David Modelli, David Malignancies
FILE REPRENCE: 014058-01440203
CURRENT FILING DAME: 2000-03-01
PRIOR FILING DAME: 2000-03-01
PRIOR PLING DAME: 2000-03-01
PRIOR PLING DAME: 2000-04-28
PRIOR PLING DAME: 2000-04-28
PRIOR PLING DAME: 2000-04-28
PRIOR PLING DAME: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200, 799
PRIOR APPLICATION NUMBER: US 60/200, 999
PRIOR APPLICATION NUMBER: US 60/200, 999
PRIOR APPLICATION NUMBER: US 60/200, 999
PRIOR PLING DAME: 2000-05-04

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APPLICANT: McMeill, Patricia Dianne
APPLICANT: McMeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-057-475B-453
Sequence 453, Application US/10057475B
Publication No. US200400206BA1
GENERAL INFORMATION:
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Clapper, Jonathan David
Wang, Aijun
Ordonez, Nadia
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; OTHER INFORMATION: n = g, a, c or
US-10-057-475B-299
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Publication No. US20040002068A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (1)...(182)
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                                                                                                                                                                                                        18-10-400-862-3607, Application US/10040862
Publication No. USG003007393641
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Manion, Jane
APPLICANT: Manion,
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89.5%; Pred. No. 3.9e+02;
tive 0; Mismatches 2; Indels 0
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US-10-057-475B-299
; Sequence 299, Application US/10057475B
    100 AGCTGCAAACAGTACAATG 118
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; OTHER INFORMATION: n=A,T,C or G
US-10-040-862-3607
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Best Local Similarity 89.5
Matches 17; Conservative
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ORGANISM: Homo sapiens
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US-10-154-884B-299
Sequence 299, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
CURRENT APPLICATION NUMBER: US/10/154,884B
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           PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,201
PRIOR PELING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION UNMERS: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-05-03
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-04
PRIOR PELING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-07
PRIOR PILING DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(182)
OTHER INFORMATION: n = g, a, c or t
US-10-057-475B-3607
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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LENGTH: 182
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Sequence 3607, Application US/10057475B

Publication No. US20040002068A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Clapper, Jonathan David

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David

APPLICANT: Mannion, Jane

APPLICANT: Mannion, Jane

APPLICANT: Moneill, Patricia Dianne

APPLICANT: Carter, Lauren

APPLICANT: Carter, 
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TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2000-10-22
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/212,903
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-08-03
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Post Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0.
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NAME/KEY: misc feature

OCTION: (1)...(182)

OCHER INFORMATION: n = g, a, c or t

US-10-057-475B-453
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -475B-3607
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GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Marc W.
APPLICANT: Mannion, Jane
APPLICANT: Corrisa Corporations and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Malignancies
FILE REFERENCE: 0.14058-0.1321US
CURRENT FILING DATE: 2.000-03-01
PRIOR APPLICATION NUMBER: US 60/120,479
PRIOR APPLICANTION NUMBER: US 60/200,545
PRIOR APPLICANTION NUMBER: US 60/200,545
PRIOR APPLICANTION NUMBER: US 60/200,799
PRIOR APPLICANTION NUMBER: US 60/200,799
PRIOR FILING DATE: 2.000-04-28
PRIOR APPLICANTION NUMBER: US 60/200,799
PRIOR FILING DATE: 2.000-05-04-18
PRIOR FILING DATE: 2.000-05-04-14
PRIOR FILING DATE: 2.000-05-04-14
PRIOR FILING DATE: 2.000-05-07-14
PRIOR APPLICANTION NUMBER: US 60/222,903
PRIOR PLING DATE: 2.000-05-06-03
PRIOR PLING DATE: 2.000-05-06-03
PRIOR PLING DATE: 2.000-05-06-03
PRIOR PLING DATE: 2.000-06-03
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PRIOR PLENCED DE PL
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Publication No. US20040175739A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Algate, Paul A.
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
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89.5%; Pred. No. 3.9e+02;
tive 0; Mismatches 2;
                                                                                                                               Sequence 3607, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-3607
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Best Local Similarity 89.59
Matches 17, Conservative
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LOCATION: (1)...(182)
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ORGANISM: Homo sapiens
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US-10-764-324-299
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APPLICANT: Reter, Marc W.
APPLICANT: Reter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE BEFERENCE: 014068-013521US
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,004
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 
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                                                                                                                                                                                                                                                                                                                                                       Length 182;
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 453, Application US/10154884B
Publication No. US20040005561A1
; GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
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LOCATION: (1)...(182)

CUTHER INFORMATION: n = g, a, c or t

US-10-154-8848-453
                                                                                                                                                | NAME/KEY: misc_feature
| LOCATION: (1)...(182)
| CTHER INFORMATION: n = g, a, c or
US-10-154-8848-299
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ORGANISM: Homo sapiens
                                      TYPE: DNA ORGANISM: Homo sapiens
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LENGTH: 182
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APPLICANT: Adgret, Paul A.
APPLICANT: Adgret, Paul A.
APPLICANT: Adgret, Paul A.
APPLICANT: Adgret, Paul A.
APPLICANT: Adgret, Marc
APPLICANT: Adgret, Marc
APPLICANT: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Malignancies
TITLE OF INVENTION: Homedological Malignancies
FILES APPLICANTON: Homedological Malignancies
FILES APPLICANTON HOMER: US/10/040,862
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR APPLICATION NUMBER: US/00/03-01
PRIOR APPLICATION NUMBER: US/00/03-01
PRIOR APPLICATION NUMBER: US/00/03-01
PRIOR APPLICATION NUMBER: US/00/03-01
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US/00/20,084
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US/00/20,084
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/00/20,084
PRIOR PLING DATE: 2000-07-14
PRIOR PLING D
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        PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR PILING DATE: 2000-05-22
PRIOR PAPLICATION NUMBER: US 60/218,950
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 453
LENGTH: 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3607, Application US/10764324 Publication No. US20040175739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(182)

OTHER INFORMATION: n = A,T,C or G
US-10-764-324-453
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NOAME/FEY: unsure
LOCATION: (54)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-10-764-324-3607
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GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Manion, Jane

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-0132004

FILE REFERENCE: 014058-012304

CURRENT FILING DATE: 2004-01-11-06

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 182
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CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
PRIOR PILING DATE: 2001-11-06
PRIOR PLING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-17
PRIOR PLING DATE: 2000-03-17
PRIOR PLING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-29
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-07
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PAPLICATION NUMBER: US 60/200,999
APPLICATION UNMBER: US 60/202,084
APPLICATION NUMBER:
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i LOCATION: (1)...(182)
CTHER INFORMATION: n = A,T,C or G
US-10-764-324-299
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ORGANISM: Homo sapiens
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APPLICANT: Coriza Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE REPRENCE: Old 588-013500US
TITLE REPRENCE: Old 588-013500US
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-04
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-0
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Pred. No. 4.1e+02;
0; Mismatches 2;
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VS-10-057-475B-5819
VS-40-ence 5819, Application US/10057475B
Publication No. US20040002068A1
                                                                                                                                          US-10-040-862-5819
Sequence 5819, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Garger, Alexander
APPLICANT: Algate, Paul A.
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100 AGCTGCAAACAGTACAATG 118
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Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
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ORGANISM: Homo sapiens
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LOCATION: (264)
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REPRENEUR: 2007.001200
CURRENT FILING DATE: 2001.03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/120,459
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-04-08
PRIOR PILING DATE: 2000-04-08
PRIOR PILING DATE: 2000-04-08
PRIOR PILING DATE: 2000-04-09
PRIOR PILING DATE: 2000-04-09
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-09-04
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-09-04
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                                                                                                                                                                                                                    Query Match
Pest Local Similarity 89.5%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0
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; OTHER INFORMATION: n=A,T,C or G
US-10-764-324-3607
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (248)
                                                   NAME/KEY: unsure
       FEATURE:
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Sequence 5819, Application US/10764324

Publication No. US20040175739A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Alexander
APPLICANT: Alexander
APPLICANT: Manion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILIAGO DATE: 2004-01-23
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FLILING DATE: 2000-03-17
PRIOR FLILING DATE: 2000-04-27
PRIOR FLILING DATE: 2000-04-27
PRIOR PLILING DATE: 2000-04-29
PRIOR FLILING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR FLILING DATE: 2000-04-28
PRIOR PLILING DATE: 2000-04-28
PRIOR PLILING DATE: 2000-05-04
PRIOR PLILING DATE: 2000-05-04
PRIOR FLILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218, 950
PRIOR APPLICATION NUMBER: US 60/218, 950
PRIOR APPLICATION NUMBER: US 60/218, 950
PRIOR APPLICATION NUMBER: US 60/22, 903
PRIOR PLILING DATE: 2000-07-14
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PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR PELICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR PELICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PELICATION NUMBER: US 60/200,779
PRIOR PLING DATE: 2000-04-28
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
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NAME/KEY: misc feature

LOCATION: (1)...(286)

OTHER INFORMATION: n = g, a, c or t
US-10-154-884B-5819
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                                                                                                                                                                                                              APPLICANT: Glapper, Ander APPLICANT: Glapper, Ander APPLICANT: Glapper, Ander APPLICANT: Wang, Aijun APPLICANT: Glapper, Ander APPLICANT: Glacer, Lauren APPLICANT: Carter, Cart
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Publication No. US20040005561A1
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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APPLICANT:
APPLICANT:
Corixa Corporation
TITLE OF INVENTION:
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                                                                                                                                                Mannion, Jane
Clapper, Jonathan David
Wang, Aljun
Ordonez, Nadia
Carter, Lauren
MCNelll, Patricia Dianne
Corixa Corporation
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; LOCATION: (1)...(286)

; OTHER INFORMATION: n = g, a, c or t

US-10-057-475B-5819
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US-10-154-884B-5819
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Gaps

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Sequence 6782.45692

| Sequence 6782.45692
| Publication No. US20020198362A1
| GENERAL INFORMATION:
| APPLICANT: Mainlen, Jane
| APPLICANT: Alexander |
| APPLICANT: Alexander |
| APPLICANT: Alexander |
| APPLICANT: Mainlen, Jane
| TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES |
| PRIOR APPLICATION NUMBER: 60/190,479 |
| PRIOR PILING DATE: 2000-04-28 |
| PRIOR PILING DATE: 2000-04-28 |
| PRIOR APPLICATION NUMBER: 60/200,303 |
| PRIOR PILING DATE: 2000-04-28 |
|
COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY HEMATOLOGICAL MALIGNANCIES
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           TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: HERATCLOGICAL MALIGNANCI
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR PLILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-08-03
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PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
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; ORGANISM: Homo sapiens
US-09-796-692-3925
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US-10-424-599-58096/C

US-10-424-599-58096/C

SQUENCE 58096, Application US/10424599

PUBLICATION . US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(53223) B

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER 09 SEQ ID NOS: 285684

SEQ ID NO 58096

LENGTH: 395
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                           PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/216,950
PRIOR FILING DATE: 2000-07-10
Remaining Prior Application data removed - See File Wrapper or FALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5819
LENGTH: 286
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Pred. No. 4.3e+02;
0; Mismatches 2; Indels 0
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Pred. No. 4.1e+02;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_23473C.1
US-10-424-599-58096
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LOCATION: (1)..(395)
OTHER INFORMATION: unsure at all n locations
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Publication No. US20020198362A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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NAME/KEY: unsure
LOCATION: (264)
OTHER INFORMATION: n=A,T,C or G
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NAME/KEY: unsure
LOCATION: (248)
OTHER INFORMATION: n=A,T,C or
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Best Local Similarity 89.5%;
Matches 17; Conservative C
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserva'
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US-09-796-692-3925
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PUBLICATION NO. US20030078396A1

APPLICATION NO. US20030078396A1

APPLICATION NO. US20030078396A1

APPLICANT: GALGET, Alexander

BRIOR FILING DATE: 2001.13-00.

BRIOR FILING DATE: 2001.13-00.

BRIOR FILING DATE: 2002.04-22

BRIOR FILING DATE: 2002.04-24

BRIOR FILING 
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                                                                                                                        Query Match 79.0%; Score 15.8; DB 14; Length 482; Best Local Similarity 89.5%; Pred. No. 4.4e+02; Matches 17; Conservative 0; Mismatches 2; Indels 0.
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US-10-057-475B-3925
; Sequence 3925, Application US/10057475B
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                ORGANISM: Homo sapiens
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US-10-040-862-6782
                        / UK-10-040-862-3925
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APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Paul A.
APPLICANT: Adgret. Marc

APPLICANT: Compositions and Methods for the Detection, Disgnosis and Therapy
TITLE OF INVENTION: Compositions and Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICANTON NUMBER: US/10/400,862
CURRENT APPLICANTON NUMBER: US/20/400,862
CURRENT APPLICANTON NUMBER: US/20/000,303
PRIOR PALING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR PAPLICANTON NUMBER: US 60/223, 416
PRIOR APPLICANTON NUMBER: US 60/223, 416
PRIOR P
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PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-07
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Publication No. US20030078396A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-796-692-6782
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LENGTH: 482
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corriva Corpositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Composition Malagnancies
FILE REPRENCE: 014058-013521US
CURRENT FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
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89.5%; Pred. No. 4.4e+02;
ive 0; Mismatches 2;
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-22
PRIOR PRILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 10979 NOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 6782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
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APPLICATION NUMBER: US 60/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3925, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AGCTGCAAACAGTACAATG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.0
Best Local Similarity 89.5
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-057-475B-6782
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                                                GENERAL INFORMATION

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Calger, Jonathan David

APPLICANT: Clapper, Jonathan David

APPLICANT: Carter, Lauren

APPLICANT: Carter, Lauren

APPLICANT: Coriosia Corporation

APPLICANT: Coriosia Coriosia

PRIOR APPLICANT: CONOUSIA CORIOSIA CORIOSIA

PRIOR PLING DATE: 2000-03-01

PRIOR APPLICANT: CONOUSIA CORIOSIA

PRIOR PLING DATE: 2000-05-04

PRIOR P
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; Sequence 6782, Application US/10057475B
; Publication No. US20040002068A1
; Publication No. US20040002068A1
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannon, Jane
; APPLICANT: Gaiper, Jonathan David
; APPLICANT: Gaiper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Garber, Jouren
; APPLICANT: Garber, Lauren
; APPLICANT: Garber, Lauren
; APPLICANT: Carixa Corporation
; APPLICANT: Carixa Corporation
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hemataclogical Malignancies
; TITE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
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79.0%; Score 15.8; DB 16; Length 482;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 AGCTGCAAACAGTACAATG 118
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                            No. US20040002068A1
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Corisa Corporation
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
ITILE OF INVENTION: UNMERS: US/10/764,324
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT APPLICATION NUMBER: US/10/40,862
PRIOR FILING DATE: 2000-01-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FLIING DATE: 2000-03-17
PRIOR FLIING DATE: 2000-03-17
PRIOR FLIING DATE: 2000-03-17
PRIOR FLIING DATE: 2000-04-27
PRIOR FLIING DATE: 2000-04-27
PRIOR FLIING DATE: 2000-04-27
PRIOR FLIING DATE: 2000-06-01
PRIOR FLIING DATE: 2000-06-01
PRIOR FLIING DATE: 2000-06-01
PRIOR FLIING DATE: 2000-05-01
PRIOR FLIING DATE: 2000-05-01
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| Publication No. US20040175739A1
| Publication No. US20040175739A1
| GENERAL INFORMATION |
| APPLICANT: Galger, Alexander |
| APPLICANT: Algate, Paul A. |
| APPLICANT: Mander |
| APPLICANT: Marchine, Jane |
| APPLICANT: Retrer, Jane |
| APPL
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
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89.5%; Pred. No. 4.4e+02;
tive 0; Mismatches 2;
                         Sequence 3925, Application US/10764324
Publication No. US20040175739A1
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Best Local Similarity 89.55
Matches 17; Conservative
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CORGANISM: Homo sapiens
US-10-764-324-3925
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Marcher, Malgnancies
TITLE OF INVENTION: Hematological Malignancies
TITLE PEPERBURGE: 014058-013521US
CURRENT APPLICATION UNMER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PELING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-01
PRIOR PELING DATE: 2000-05-02
PRIOR PELING DATE: 2000-05-04
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-08-04
PRIOR PILING DATE: 2000-08-04
PRIOR PILING 
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Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 11290 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3925 LENGTH: 482
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Pred. No. 4.4e+02;
0; Mismatches 2;
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Pred. No. 4.4e+02;
0; Mismatches 2;
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Publication No. US20040005561A1
GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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Best Local Similarity 89.5%;
Matches 17; Conservative (
                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-154-884B-3925
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CORGANISM: Homo sapiens
US-10-154-884B-6782
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US-10-764-324-3925
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Marc
APPLICANT: Corixa Corporation
APPLICANT: Construction
APPLICANT: Marc
APPLICANT: Manual Malignancies
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                                                                                                        Length 492;
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                                                                                                        Score 15.8; DB 9;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TILLE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR PELICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-29
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-07
PRIOR PRIO
                                                                                                        Query Match
Best Local Similarity 89.5%; Pred. No. 4.4e
Matches 17; Conservative 0; Mismatches
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US-10-057-475B-2741
; Sequence 2741, Application US/10057475B
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Sequence 2741, Application US/10040862

Publication No. US20030078396A1

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AGCTGCAAACAGTACAATG 118
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US-10-040-862-2741
; ORGANISM: Homo sapiens
US-09-796-692-2741
                                                                                                                    Query Match
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Sequence 2741, Application US/09796692

SEQUENCAL INCORMATION:
SEQUENCE CALL ON US20201993621

SERENAL INCORMATION:
APPLICANT GAIGST. Paul A.
APPLICANT Algate, Paul A.
APPLICANT:
MILL OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
STIOR APPLICATION NUMBER: 60/190, 479
FRIOR APPLICATION NUMBER: 60/190, 479
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR APPLICATION NUMBER: 60/200, 304
FRIOR FILING DATE: 2000-05-01
FRIOR APPLICATION NUMBER: 60/202, 304
FRIOR FILING DATE: 2000-05-04
FRIOR APPLICATION NUMBER: 60/222, 903
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2
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    PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PILING DATE: 2000-05-04
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Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AGCTGCAAACAGTACAATG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-764-324-6782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 35
US-09-796-692-2741
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LENGTH: 492
TYPE: DNA
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Sequence 2741, Application US/10764324
Publication Vo. US20040175739A1
Publication No. US20040175739A1
Publication No. US20040175739A1
Publication No. US20040175739A1
APPLICANT: Gaiger, Alexander
APPLICANT: Adjate, Marc
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
APPLICANT: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REPERENCE: 014068-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/218,950
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PRIOR PELLING DATE: 2001-11-06
PRIOR PELLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-03-17
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,99
PRIOR PELLING DATE: 2000-05-01
PELLING DATE: 2001-05-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; Score 15.8; DB 16; alarity 89.5%; Pred. No. 4.4e+02; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AGCTGCAAACAGTACAATG 118
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US-10-154-884B-2741
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Best Local Similarity
Matches 17; Conserv
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Sequence 2741, Application US/10154884B

Publication No. US20040005561A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jame

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Compositions and Malignancies

FILE REFERENCE: 014058-0135210S

CURRENT APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-03-17
                                                                                         APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Carter, Lauren
APPLICANT: Orater, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
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FILE REFERENCE: 014058-0144058

CURRENT APPLICATION NUMBER: US/10/057,4758

CURRENT FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/180,479

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR PELING DATE: 2000-04-28

PRIOR PILING DATE: 2000-05-01

PRIOR PILING DATE: 2000-05-01

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 2000-05-01

PRIOR PILING DATE: 2000-05-01

PRIOR PILING DATE: 2000-05-01

PRIOR PILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/206,201

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-03

PRIOR PILING DATE: 2000-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 AGCTGCAAACAGTACAATG 118
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               Publication No. US20040002068A1
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ORGANISM: Homo sapiens

US-10-057-475B-2741
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US-101.427-963-58097/C
US-10-437-963-58097/C
US-10-437-963-58097/Application US/10437963
Sequence 58097, Application US/10437963
Publication No. US20040123343A1
Sequence 58097, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Broukharcov, Andrey A.
APPLICANT: Broukharcov, Andrey A.
APPLICANT: Li, Ping
APPLICANT: Li, Ping
ITILE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT PILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 58097
LENGTH: 1048
LENGTH: 1048
LENGTH: 1048
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APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Tramamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yu, H.
APPLICANT: Xu, H.
APPLICANT: Stramamoto, Robert
APPLICANT: Stramamoto, Robert
APPLICANT: Stramamoto, Robert
APPLICANT: Stramamoto, Robert
APPLICANT: Number: Us/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PRILING DATE: 2006-03-21
PRIOR PLING DATE: 2006-03-21
PRIOR PLING DATE: 2006-03-21
                                                                                                                               Gaps
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                                                                                                                               Indels
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Best Local Similarity 89.5%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 2;
                                                                              Score 15.8; DB 17;
Pred. No. 4.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_59846C.1
US-10-437-963-58097
         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_96950C.1
US-10-437-963-99107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5046, Application US/10282122A
Publication No. US20640629129A1
PUBLICANT: Wang, Liangsu
APPLICANT: Wamdio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    945 AGTCGACAACAGTACAATG 927
                                                                                                                                                                                                                         231 AGTCGCCAACAGTACATIG 213
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                                                                                                                                                                               1 AGTCGCAAACAGTACAATG 19
                                                                                Query Match
Best Local Similarity 89.5%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -10-282-122A-9046
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FEATURE:
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; Sequence 99107, Application US/10437963
; Publication No. US20040123343A1
; Fublication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Calou, Yihua
    APPLICANT: Calou, Yihua
    APPLICANT: Calou, Yongwei
    APPLICANT: Boukharco, Andrey A.
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: 18-21 (53221)
    CURRENT TILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 99107

LENGTH: 536

LENGTH: 536

LENGTH: 536
                                                                                                                                                                                                                                                                                                                                                        Sequence 12273.
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Best Local Similarity 89.5%; Pred: No. 4.40+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0
                                                                                                             Query Match

19.0%; Score 15.8; DB 17; Length 492;
Best Local Similarity 89.5%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: MAP TO CHRIZ.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPLANAN HIT: A1797907.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: 911365028, EVALUE 0.00e+00
OTHER INFORMATION: SWISSPROT HIT: P24731, EVALUE 8.10e+00
US-10-029-386-13273
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                                                                                                                                                                                                                                             100 AGCTGCAACAGTACAATG 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                               TYPE: DNA ORGANISM: Homo sapiens
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US-10-437-963-99107/c
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US-10-029-386-13273
                                                             LENGTH: 492
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US-10-027-0283-02-112288/c

Sequence 112288, Application US/10027632

Publication No. US20020198371A1

Publication No. US20020198371A1

Publication No. US20020198371A1

THE CORRENT WANG, DAVIG G,

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108027.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PELLING DATE: 2000-07-12

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-04-20

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 2000-03-29

PRIOR PELLING DATE: 1999-09-11-23

PRIOR PELLING DATE: 1999-09-28

PRIOR PELLING DATE: 1999-09-28

PRIOR PELLING DATE: 1999-09-28

PRIOR PELLING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

SOFFWARE FREING DATE: 1999-08-08

SOFFWARE FREING DATE: 1990-08-08

SOFFWARE FREING DATE: 1990-08-08

SOFFWARE FREING DATE: 1990-08-08

SOFFWARE FREING
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                                                                                                                               JS-10-027-632-112288/c
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US-10-027-632-112288/c
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US-10-027-632-112288
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PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PILING DATE: 2000-05-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PILING DATE: 2000-09-06

PRIOR PILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

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Patent No. US20020144047A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-10-282-122A-9046
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; ORGANISM: Arabidopsis thaliana
US-09-887-576-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brown, D. APPLICANT: Chang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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JULIO 1207-132-112289/C
GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
WANG, DAVIG G
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/196,066
PRIOR APPLICATION NUMBER: US 60/196,066
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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419 AGTTGCAAACAGAACAATG 437

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Sequence 170, Application US/10158844

Fublication No. US20040029118A1

GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                   Sequence 170, Application US/08961527
Sequence 170, Application US/08961527
Sublication No. US20020032233A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS: ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STRIE: Maryland
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79.0%; Score 15.8; DB 8; Length 8876;
Best Local Similarity 89.5%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches '2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
ATTORA APPLICATION NUMBER: BASIADI
APPLICATION NUMBER: 36,373
REGISTRATION NUMBER: 36,373
REG
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                  1 AGTCGCAAACAGTACAATG 19
                                                                              51 AGTCGCAAACAGCGCAATG 69
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US-10-158-844-170/c
                                                                                                                                                                                              RESULT 49
US-08-961-527-170/c
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US-10-320-797-329

Sequence 329, Application US/10320797

Publication No. US20040014955A1

GENERAL INFORMATION:

APPLICANT: Excentin, Alexey M.

APPLICANT: Zamudio, Carlos

TITLE OF INVENTION: NETHODS OF USE

TITLE OF INVENTION: NETHODS OF USE

TITLE OF INVENTION: NUMBER: US/10/320,797

CURRENT FILING DATE: 2002-12-16

PRIOR PPLICATION NUMBER: 60/341,261

PRIOR PPLICATION NUMBER: 60/341,261

PRIOR PLING DATE: 2001-12-17

NUMBER OF SEQ ID NOS: 3361

SSO ID NO 329

LENGTH: 5238
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 41469/c

Sequence 41469/c

Sequence 41469/c

Sequence 41469/c

Septence 41469/c

Enblication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bubazuk, Brad

APPLICANT: Brad

APPLICANT: Bransauk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: 20163221)

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 41469

LERGHH: 3346

TERGHH: 3346
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79.0%; Score 15.8; DB 17; Length 3546;
Best Local Similarity 89.5%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
                                                                                         Query Match

79.0%; Score 15.8; DB 15; Length 2759;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_44810C.1
US-10-437-963-41469
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APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/08/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 170, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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HP Vectra 486/33
SYSTEM: MSDOS version 6.2
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                                                                                                                                                                  Query Match
79.0%; Score 15.8; Dest Local Similarity 89.5%; Pred. No. 90; Matches 17; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILLING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO S85
LENGTH: 1281
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COMPUTER: HP Vectra 466/33
OPERATING SYSTEM: MSDOS version 6
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                       US-09-328-352-890
; Sequence 890, Application US/09328352
; Patent No. 6562958
; GENBRAL INFORMATION:
                                                                                                                                                                                                                                                                   315 GTGGCAAACATTACAATGG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA; ORGANISM: Acinetobacter baumannii
US-09-328-352-890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 GreeceAcarracaares 518
                                                                                                                                                                                                                                           2 GTCGCAAACAGTACAATGG 20
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                               ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-961-527-170/c
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                                                                                                                         JS-09-543-681A-585
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                                                                                                TYPE: DNA
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Patent No. 6699703

GENERAL INFORMATION:

TITLE OF INVENTION: Determined and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: Preumoniae for Diagnostics and Therapeutics

TITLE OF INVENTION: PartHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

CURRENT FILING DATE: 1998-06-30

PRIOR PILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR PILING DATE: 1998-05-12

NUMBER OF SEQ ID NOS: 5322

LENGTH: 906

LENGTH: 906
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Patent No. 6605709
GENERAL INFORMATION:
FILL DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
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1, Appli
5, Appli
5, Appli
604, App
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                                                                        US-09-521-220-10
US-09-710-279-4250
US-09-710-279-11
US-08-155-331-12
US-08-424-022-12
                                                                                                                                                                    US-08-424-017B-12
PCT-US93-11696-12
US-09-710-279-4145
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US-09-221-017B-604
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US-09-693-542-47
US-09-620-312D-128
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US-09-295-028-47
US-09-106-582-47
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US-08-121-057-3
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Best Local Similarity 89.5
Matches 17; Conservative
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249 cechancaechchares 233

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Brookes, A. Anders

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RESULT 8
US-08-781-986A-16
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US-09-270-767-21230/c
; Sequence 21230, Application US/09270767
; Batent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION UNDRER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21230
LENGTH: 427
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Sequence 5948, Application US/09270767

Factorice 5948, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;

FILE REFERENCE: File Reference: 7326-094

CURRENT PAPLICANION NUMBER: US/09/270,767

CURRENT FILIG DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE PATENTIN Ver. 2.0

SEQ ID NO 5948
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1e+02;
hes 2; Indels 0
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                                                                                                                                                                                                                                                            Score 15.8; DE
Pred. No. 1e+02
pred. Mismatches
REGISTRATION NUMBER: 36,373
REGISTRATION NUMBER: 98340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 170:
SEQUENCE CHARACTERISTICS:
LENGTH: 8876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                  4731 GTCGCAAAAGAACAATGG 4713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5948
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Best Local Similarity 89.5%;
Matches 17; Conservative
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Best Local Similarity
Matches 16; Conserv
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US-08-961-527-170
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Best Local Similarity
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4 CGCAAACAGTACAATGG 20

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TITLE OF INVENTION:
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTON: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                                                                         COMPUTE: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP voctra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOSTWARE: ASCII TEAXL
CURRENT APPLICATION DATA:

RPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFCATION: CURNOWN->
PRIOR APPLICATION NUMBER: 06/09,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

APPLICATION NUMBER: 08/781,986

APPLICATION NUMBER: 08/781,986

ATORNEY/AGET INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELEBHOME: (340) 314-1224

TELEBHOME: (340) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICE:
SEQUENCE CHARACTERISTICE

LENGTH. 13086 hase Daire
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
Sequence 16, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 13086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 94.1
Matches 16; Conservative
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RESULT 10
US-09-328-352-2264/c
US-09-328-352-2264/c
Sequence 2264, Application US/09328352
Fatent No. 656258
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REPRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
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Becart No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: DEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: UNDER: US/09/134,001C

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRICR APPLICATION NUMBER: US 60/064,964

PRICR APPLICATION NUMBER: US 60/065,779

PRICR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1596

LENGTH: 1278
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Patent No. 6703492
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.0%; Score 15.2; DB 4; Length 756; Best Local Similarity 85.0%; Pred. No. 1.7e+02; Matches 17; Conservative 0; Mismatches 3; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1596
     630 AGTCGCAAGCAGTTCAGTGG 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 AGTCGCAAACAGTTTAATTG 148
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US-09-134-001C-1596
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US-09-710-279-109
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Sequence 34579, Application US/09513999C

Patent No. 6783611

Patent No. 6783611

APPLICANT: DWAGERT, A.

APPLICANT: DWAGERT, A.

ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPEL REFERENCE: 59.032.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1090-02.24

PRIOR FILING DATE: 1099-02.26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 34579

LUMBER OF SEQ ID NOS: 36681

SEQ ID NO 34579
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77.0%; Score 15.4; DB 4; Length 13086;
Best Local Similarity 94.1%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                   ZIP: ZUBJU
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV Vectra 486/33
COMPUTER: MSDOS Version 6.2
                                                                                                                                                                          COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bb.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
EENGTH: 13096 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2194 AATCGCAAACAGTACAA 2210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 13086 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
US-08-781-986A-16
                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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0; Gaps
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Sequence 9, Application US/09026001A
Patent No. 6413760
GENERAL INFORMATION:
APPLICANT: Boodhoo, Amechand
APPLICANT: Seave, Jashir
APPLICANT: Shaw, Gray
ITILE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A COBRA VENOM
TITLE OF INVENTION: HIGHLY PURIFIED MOCARHAGIN, A CORPETED: 2 CORRESPONDED ADDRESSER: Genetics Institute, Inc.
STREET: Gambridge
STATE: Massachusetts
COMPUTER: 18 PC Compatible
COMPUTER: 18 PC COMPASSION
SOFTWARE: PREED-1998
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 015/09/026,001A
FILING DATE: 18 PEBB-1998
CURRENT APPLICATION 1498-8214
INPORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LEBROHNE: G(17) 876-8851
INPORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LEBROHNE: APPLICATION: A SEAL A TELEBRONE: (617) 876-8851
INPORMATION FOR SEQ ID NO. 9:
SEQUENCE CHARACTERISTICS:
LEBROHNES CHARACTERI
                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: synthetic; CTHER INFORMATION: nucleic acid sequence US-09-710-279-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 76.0%; Score 15.2; DB 4; Length 1278; Best Local Similarity 85.0%; Pred. No. 1.8e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2184 Arredcaaacachaaared 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AGTCGCAAACAGTTTAATTG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AGTCGCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTCGCAAACAGTACAATGG 20
                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-11-09
                                         NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
LENGTH: 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-026-001A-9
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REGION 14

18-09-056-01A-17/C

18-09-01A-17/C

18-09-056-01A-17/C

18-09-01A-17/C

18-09-0
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Gaps

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3; Indels

Length 168575;

us-10-050-189a-7.rni

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Sequence 1, Application US/08620605D
Sequence 1, Application US/08620605D
Sequence 1, Sedent No. Sedent No. Sedent No. Sedent No. Sedent No. Sedent No. TELS OF INFORMATION:
APPLICANT: AFATSURA, HIROYUKI
APPLICANT: KAWAI, ERI
TITLE OF INVENTION: GENE PARTICIPATING IN THE MECHANISM OF
TITLE OF INVENTION: SECRETION OF ESTERASE
NUMBER OF SEQUENCES:
ADDRESSER: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STREET: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 15; DB 2; Length 4465; 100.0%; Pred. No. 2.4e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IDAPPY disk
COMPUTER: Floppy disk
COMPUTER: IDAPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,605D
FILING DATE: 22-MAR-1996
CLASSIFICATION: 435
ATTONNEY/AGNET INFORMATION:
NAME: STENSON, LEONARD R
REGISTRATION NUMBER: 30,330
REPERENCE/DOCKET NUMBER: 30,330
REPERENCE/DOCKET NUMBER: 30,330
RELEPRANICATION NUMBER: 30,330
RELEPRANICATION NUMBER: 30,330
RELEPRANICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4465 Dase pairs
TYPE: MINCHESS: double
                                                                                                                                                Query Match 76.0%; Score 15.2; DB 4; Best Local Similarity 85.0%; Pred. No. 2.5e+02; Matches 17; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                            114928 AGTCACAAATAGTAAATGG 114947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serratia marcescens Sr41
                                                                                                                                                                                                                                          1 AGTCGCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-005-232A-1
; Sequence 1, Application US/09005232A
; Patent No. 5922568
                               LOCATION: (127009)...(127130)
NAMEY: CDS
| LOCATION: (128910)...(129139)
US-09-426-290-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4242 CGCAAACAGTACAAT 4256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 15; Conserv
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USA
            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                           RESULT 18
US-08-620-605D-1
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Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT FILING DATE: 10500-11-09
PRIOR APPLICATION NUMBER: 60164,258
PRIOR PELING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4314
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: nucleic acid sequence US-09-710-279-3876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
CTHER INFORMATION: Description of Artificial Sequence: synthetic
CTHER INFORMATION: nucleic acid sequence
US-09-710-279-4314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                          Query Match 76.0%; Score 15.2; DB 4; Length 3172; Best Local Similarity 85.0%; Pred. No. 1.9e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 15.2; DB 4; Length 3172; 85.0%; Pred. No. 1.98+02; vative 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher:
TILE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2001.000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                   501 AGTCGCAAACAGTTTAATTG 520
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                                                                                                                                                                                       1 AGTCGCAAACAGTACAATGG 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 85.0°
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 168575
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                        US-09-710-279-4314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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NAME/KEY:
LOCATION:
NAME/KEY:
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Gaps

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US-09-134-001C-2315

Sequence 2315, Application US/09134001C

Sequence 2315, Application US/09134001C

Sequence 2315, Application US/09134001C

GENERAL INFORMATION:

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: UNMBER: US/09/134,001C

TITLE OF INVENTION: UNMBER: US/09/134,001C

CURRENT FILING DATE: 1997-10-08

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

SEQ ID NOS: 5674

LENGTH: 192
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US-09-270-767-2529/C
US-09-270-767-2529/C

| Sequence 2529, Application US/09270767
| Patent No. 670349|
| GENURAL INFORMATION:
| APPLICANT: Homburger et al.
| TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
| FILE REFERENCE: File Reference: 7326-094
| CURRENT APPLICATION NUMBER: US/09/270,767
| CURRENT FILING DATE: 1999-03-17
| NUMBER OF SEQ ID NOS: 62517
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 2529
| LENGTH: 272
| TYPE: DNA
| OSCANISM: Drosophila melanogaster
US-09-270-767-2529
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                         Query Match 75.0%; Score 15; DB 4; Length 580073; Best Local Similarity 100.0%; Pred. No. 3.1e+02; Matches 15; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 4; Length 272;
Pred. No. 2.5e+02;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 17811, Application US/09270767; Patent No. 6703491
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA; CRANISM: Staphylococcus epidermidis US-09-134-001C-2315
                                                                                                                                                                                                                                   160781 CAAACAGTACAATGG 160795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 GTCGCAAAAGTACAAGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GTCGCAAACAGTACAATG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.0%;
                                                                                                                                                                        6 CAAACAGTACAATGG 20
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Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 23
US-09-270-767-17811/c
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Sequence 1, Application US/08545528D

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION NUMBER: US/08/545,528D

CURRENT FILING DATE: 1995-10-19

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1
   GENERAL INFORMATION:

APPLICANT: SHIBATANI, TAKEJI
APPLICANT: SHIBATANI, TAKEJI
APPLICANT: SAWAI, ERI
TITLE OF INVENTION: GENE PARTICIPATING IN THE MECHANISM OF
TITLE OF INVENTION: SECRETION OF ESTERASE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE: BIRCH
STRET: PO BOX 747
CITY: FALLS CHURCH
STRET: PO BOX 747
CITY: FALLS CHURCH
STRET: PO BOX 747
COMPUTER: DAY
ACUMINEN: LEM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEALTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,232A
FILING DATE:
APPLICATION NUMBER: US/09/005,232A
FILING DATE:
APPLICATION NUMBER: US/09/005,232A
FILING DATE:
APPLICATION NUMBER: US/0300
REFERENCE/DOCKET NUMBER:
TELEPHONE: (703)-205-8000
INPORMATION POR SEQ ID NO: 1:
SEQUENCE CHARACTER SETILS:
LENGTH: 4547 base pairs
TTELEPHONES: Qouble
TREATER DATA
THERE THE COMPUTER: THE COMPATIBLE
THERE THE COMPUTER: THE COMPATIBLE
THERE THE COMPUTER: THE COMPATIBLE
TELEPHONE: (703)-205-8000
TELEFAX: (703)-205-8000
TELEFAX: (703)-205-8000
TELEGRAX: (703)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.0%; Score 15; DB 2; Length 4547; Best Local Similarity 100.0%; Pred. No. 2.5e+02; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
STRAIN: Serratia marcescens Sr41
US-09-005-232A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Mycoplasma genitalium
US-08-545-528D-1
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GENERAL INFORMATION:
APPLICANT: SHIBAT
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LENGTH: 580073
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US-08-545-528D-1
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Sequence 4228, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT FILING DATE: 2000-11-09
PRIOR PAPLICATION NUMBER: 60/164,258
PRIOR PLEATION DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: patentin Ver. 2.1
SEQ ID NO 4298
LENGTH: 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3640, Application US/09710279

Retent No. 6703492.

Retent No. 6703492.

Retent No. 6703492.

APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
RIOR PILING DATE: 1999-11-09
SOFTWARE: PRECENTION OF SEQ ID NOS: 4472
SOFTWARE: PRECENTIN Ver. 2.1
SEQ ID NO 3640
LENGTH: 3638
                                                                                                                                                   Gaps
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74.0%; Score 14.8; DB 4; Length 3446;
Best Local Similarity 88.9%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0.
                                                                                                 Length 924;
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                                                                                                                                              2; Indels
                                                                                            Score 14.8; DB 3;
Pred. No. 2.7e+02;
0; Mismatches 2;
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; OTHER INFORMATION: Description of Artifi,
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3640
                  ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2719 GACGCATACAGTACAATG 2736
                                                                                                                                                                                                                             860 GACGCATACAGTACAATG 877
                                                                                                                                                                                             2 GTCGCAAACAGTACAATG 19
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                                                                                         Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
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| Patent No. 6380370
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| TITLE OF INVENTION: BPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BPIDERALDIS FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT PREPARE: GTC-007
| CURRENT PAPLICATION NUMBER: US/09/134,001C
| CURRENT PAPLICATION NUMBER: US 60/064,964
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-11-08
| PRIOR FILING DATE: 1997-01-14
| SEQ ID NOS: 5674
| TYPE: DNA
| TYPE: DNA
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APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17811
LENGTH: 272
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Retent No. 6703492

RETENT NO. 6703492

GENERAL INFORMATION:
APPLICANT: KIRWERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P19486002

CURRENT APPLICATION NUMBER: US/09/710,279

PRIOR PILLING DATE: 2000-11-09

PRIOR FILLING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: Patentin Ver: 2.1

LENGTH: 861
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74.0%; Score 14.8; DB 4; Length 861;
Best Local Similarity 88.9%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                    ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 GTCGCAAAAGTACAAGG 252
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Best Local Similarity 88.9%;
Matches 16; Conservative
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RESULT 31
US-09-134-000C-875
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§ Sequence 30016, Application US/09270767

§ GENERAL INFORMATION:

§ APPLICANT: Homburger et al.

§ TILLE REFERENCE: File Reference: 7326-094

§ CURRENT PAPLICANTION NUMBER: US/09/270,767

§ NUMBER OF SEQ ID NOS: 62517

§ SEQ ID NO 30016

§ LENGTH: 656
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Sequence 13942, Application US/09270767

Parent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Notleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767
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                                                        RESULT 28
US-09-713-273A-15/C
Sequence 15, Application US/09713273A
Patent No. 6620987
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: BALLEN, Steve
TITLE OF INVENTION: STARCH RI PHOSPHORYLATION PROTEINS
FILE REFERENCE: BBL188 US CIP
CURRENT APPLICATION NUMBER: US/09/713,273A
CURRENT FILING DATE: 1998-04-09
FRIOR FILING DATE: 1998-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR APPLICATION NUMBER: PCT/US99/07639
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 1999-04-09
FRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 21
SSCTWARE: Microsoft Office 97
SSCTWARE: Microsoft Office 97
LENGTH: 4846
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116 GACGCATACAGTACAATG 133
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Best Local Similarity 88.99
Matches 16; Conservative
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CORGANISM: Zea mays
US-09-713-273A-15
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## Sequence #85, Application US/09134000C

## TITLE OF INVENTION: WOULEIC ACID AND AMINO ACID SEQUENCES RELATING TO

## TITLE OF INVENTION: WOULEIC ACID AND AMINO ACID SEQUENCES RELATING TO

## TITLE OF INVENTION: WOULEIC ACID AND AMINO ACID SEQUENCES RELATING TO

## TITLE OF INVENTION: WOULEIC ACID AND AMINO ACID SEQUENCES RELATING TO

## TITLE OF INVENTION: WOULEIC ACID AND THERAPEUTICS

## CURRENT APPLICATION NUMBER: US/09/134,000C

## PRIOR APPLICATION US/09/134,000C

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                                                                                                                                                                                                                                                                          TYPE: DNA; ORGANISM: Drosophila melanogaster US-09-270-767-13942
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13942
LENGTH: 724
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APPLICANT: Del Val, Greg
APPLICANT: Caillau, Maxime
APPLICANT: Lemauz, Peggy G
APPLICANT: Buchanan, Bob B.
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Matches 15, Conservative
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TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
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Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis sp. FEATURE: NAME/KEY.CDS LOCATION: (1)..(999)
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; NAME/KEY: CDS
; LOCATION: (42)..(1568)
US-09-043-302-10
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LENGTH: 1002
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Patent No. 6750046

GENERAL INPORMATION:
TILLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
TITLE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
TITLE OF INVENTION: PROPIED NO. 01L BODIES
FILE REFERENCE: 034547/0106

CURRENT APPLICATION NUMBER: 08/04/02

PRIOR FILING DATE: 2001-07-03

PRIOR FILING DATE: 1999-12-18

PRIOR PRILICATION NUMBER: 08/346, 783

PRIOR PRILING DATE: 1994-12-30

PRIOR FILING DATE: 1994-12-30

PRIOR FILING DATE: 1991-02-22

PRIOR FILING DATE: 1991-02-22

PRIOR FILING DATE: 1991-02-22

SOFTWARE: PARENT NUMBER: 08/366, 783

PRIOR FILING DATE: 1991-02-22

SEQ ID NOS: 55

SEQ ID NO 36

LENGTH: 100-3
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Sequence 37, Application US/09897425
Patent No. 6750046
GENERAL INFORMATION:
PAPLICANT: MOLONINY, MAURICE M.
APPLICANT: MOLONINY, MAURICE M.
APPLICANT: MOLONINY, MAURICE M.
APPLICANT: MOLONINY, MAURICE M.
APPLICANT: DALWIA, BIPIN K.
TITLE OF INVENTION: PROTEINS ON OIL BODIES
FILE OF INVENTION: PROTEINS ON OIL BODIES
FILE REFERENCE: 034547/0106
CURRENT APPLICATION NUMBER: US/09/897,425
CURRENT APPLICATION NUMBER: US/09/897,425
PRIOR FILING DATE: 1998-12-18
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Unknown Organism: Published NADPH OTHER INFORMATION: thioredoxin reductase sequence
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72.0%; Score 14.4; DB 4; Length 1002;
Best Local Similarity 93.8%; Pred. No. 4.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                          Query Match 72.0%; Score 14.4; DB 3; Length 998; Best Local Similarity 93.8%; Pred. No. 4.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels
                                              ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26
                                                                                                                                                                                                                                                                                          450 GTCGCAAACAGCACAA 435
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ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)..(999)
US-09-897-425-36
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US-09-897-425-36/c
SEQ ID NO 26
LENGTH: 998
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Sequence 2599, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BREION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09043302
| Sequence 10, Application US/09043302
| Patent No. 6617128
| GENERAL INFORMATION:
| APPLICANT: WEYER, Thomas F. APPLICANT: RUDEL, Thomas F. APPLICANT: RUDEL, Thomas F. APPLICANT: ALTERNIAGER, Sandra APPLICANT: EICKERNUAGER, Sandra APPLICANT: EICKERNUAGER, Sandra APPLICANT: GINTENNION: The AACHSION of Neisseria Cells to Human Cells TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells TITLE OF INVENTION: the Adhesion of Neisseria Cells to Human Cells CURRENT APLICATION NUMBER: US/09/043,302 CURRENT APPLICATION NUMBER: PCT/EP96/04092 EARLIER APPLICATION NUMBER: PCT/EP96/04092 | EARLIER APPLICATION NUMBER: PCT/EP96/04092 | EARLIER PLING DATE: 1995-09-18 | NUMBER OF SEQ ID NOS: 11 | SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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93.8%; Pred. No. 4.5e+02;
live 0; Mismatches 1;
PRIOR APPLICATION NUMBER: 08/846,021
PRIOR FILING DATE: 1997-04-25
PRIOR PILING DATE: 1994-035
PRIOR PEDICATION NUMBER: 08/142,418
PRIOR PEDILICATION NUMBER: 08/142,418
PRIOR FILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 55
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APPLICANT: SCHEUERPFLUG, Ina
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; LOCATION: (1555)..(2553)
US-09-897-425-48
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72.0%; Score 14.4; DB 4; Length 2307;
Best Local Similarity 93.8%; Pred. No. 4.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                               Query Match
72.0%; Score 14.4; DB 4; Length 2001;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and TITLE OF INVENTION: No. 6743619e1 Nucleic Acids and TITLE DEPENDENCE: 802 CURENT APPLICATION NUMBER: US/09/774,528 CURRENT FILING DATE: 2001-01-30 NUMBER OF SEQ ID NOS: 441 SEQ ID NO 314 LENGTH: 2307
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2598
LENGTH: 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 314, Application US/09774528 Patent No. 6743619 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-043-302-1/c
; Sequence 1, Application US/09043302
; Parent No. 6617128
; GENERAL INFORMATION:
; APPLICANT: MEYER, Thomas F.
; APPLICANT: RUDEL, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 gcaaacreracaaree 187
                                                                                                                                                                                                                                                                                                                                                                                         714 GCAAACAGAACAATGG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                     5 GCAAACAGTACAATGG 20
                                                                                                                                                                                                          ORGANISM: Proteus mirabilis US-09-543-681A-2598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang, Y. Tom Zhou, Ping Goodrich, Ping Goodrich, Ryle Liu, Chenghua Asundi, Vinod Ren, Feiyan Zhao, Qing A. Yang, Yonghong Xue, Aidong J. Wehrman, Tom Wang, Jian-Rui Wang, Durzui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , NAME/KEY: CDS
, LOCATION: (318)..(2180)
US-09-774-528-314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-774-528-314
                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
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APPLICANT WAIRS, Ungent APPLICANT WITS, Ungent APPLICANT WITS, Ungent APPLICANT SCHEMA Thomse APPLICANT SCHEMA TOWNS APPLICANT TOWNS APPLICATION NUMBER: USG-6.08

EMALIES FILLS APPLICATION NUMBER: USG-6.08

EMALIES FILLS APPLICATION NUMBER: USG-6.08

EMALIES APPLICATION NUMBER: USG-6.08

EMALICANT WOOLNEY, MULTICE APPLICATION NUMBER: USG-6.08

EMALICANT WOOLNEY, MULTICE APPLICATION NUMBER: USG-6.73

EMALICANT TILNO DATE: 1991-04-25

EMALICANT NUMBER: USG-6.73

EMALICANT NUMBER: USG-7.73

EMALIES NUMBER: USG-7.73

EMALIES NUMBER: USG-7.73

EMALIES NUMBER: USG-7.73

EMALIES NUMBER: USG-7.73

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
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                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/09897425

Facent No. 6750046

GENERAL INFORMATION:

APPLICANT: MOLONEN, MAURICE M.

APPLICANT: DALMIA, BIPIN K.

ITILE OF INVENTION: PREPARATION OF THIOREDOXIN REDUCTASE

ITILE OF INVENTION: PROTEINS ON OIL BODIES

FILE REFERENCE: 034547/0106

CURRENT APPLICATION NUMBER: US/09/897,425

CURRENT APPLICATION NUMBER: 09/210,843

PRIOR APPLICATION NUMBER: 08/366,783

PRIOR PLING DATE: 1999-12-30

PRIOR PLING DATE: 1997-04-25

FRIOR PLING DATE: 1991-12-30

PRIOR PLING DATE: 1991-12-30

PRIOR PLING DATE: 1991-12-30

PRIOR APPLICATION NUMBER: 08/366,783

PRIOR PLING DATE: 1993-11-16

PRIOR PLING DATE: 1991-02-22

NUMBER OF SEQ ID NOSE: 55

SOPTWARE: PATENTING DATE: 1991-02-22

NUMBER OF SEQ ID NOSE: 55

SOPTWARE: PATENTING DATE: 1991-02-22

NUMBER OF SEQ ID NOSE: 55

SEQUENCE: 100 NOSE: 55

FROM THE NOSE: 55
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Patent No. 6750046

GENERAL INFORMATION:
APPLICANT: MOLONEY, MAURICE M.
APPLICANT: MOLONEY, MAURICE M.
APPLICANT: DALMIA, BIPIN K.
ITILE OF INVENTION: PREPARATION OF THIOREDOXIN AND THIOREDOXIN REDUCTASE
ITILE OF INVENTION: PROTEINS ON OIL BODIES
ITILE OF INVENTION: PROTEINS ON OIL BODIES
CURRENT APPLICATION NUMBER: US/09/897,425
CURRENT APPLICATION NUMBER: 09/210,843
PRIOR PLILOM DATE: 1998-12-18
PRIOR PLILOM DATE: 1998-12-18
PRIOR PLILOM DATE: 1999-04-25

PRIOR APPLICATION NUMBER: 08/846,021

PRIOR PLILOM DATE: 1997-04-25
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                                                                 Gaps
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Query Match 72.0%; Score 14.4; DB 4; Length 3787; Best Local Similarity 93.8%; Pred. No. 4.7e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                       2 GTCGCAAACAGTACAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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US-09-897-425-53/c
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Gaps
                                                                                                                                                                                                                   TYPE: DNA
ORCANISM: Artificial Sequence
FEATURE: DNA
OTHER INFORMATION: Description of Artificial Sequence: Phaseolin
OTHER INFORMATION: promoter-oleosin thioredoxin reducatse-phaseolin
OTHER INFORMATION: terminator
OTHER INFORMATION: terminator
INCATION: (1555)..(1908)
INAME/KEY: CDS
INCATION: (2149)..(3312)
US-09-897-425-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SECUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: U.S.A.
ZIP: 20007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release-#1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A,
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT. WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper.
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
PRIOR FILING DATE: 1994-12-30
PRIOR APPLICATION NUMBER: 08/142,418
PRIOR PILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 55
SEQ ID NO SO: 150
LENGTH: 4546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-000-094-45
; Sequence 45. Application US/09000094
Patent No. 6365160
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2766 GTCGCAACAGCACAA 2751
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FRAZE, Ian
MCMILLAN, Nigel Alan John
MILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
Holland
EDWARDS, Stirling John
TITLE OF INVENTIOR: 50
CORRESPONDENCE ADDRESS: 50
CORRESPONDENCE ADDRESSES, LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                 Query Match
Best Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITATE: D.C.
COUNTER: D.C.
ZIP: 20007-5109
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DAYSTEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,004
FILING DATE: 21-Apr-1998
CLASSIFICATION: UNMBER: WO PCT/AU96/00473
FILING DATE: 26-JUJ-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISCHARTON NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELBRAX: (202) 672-5399
INFORMATION: CONTON INFORMATION:
TELBRAX: (202) 672-5399
INFORMATION: CONTON INFORMATION:
SEQUENCE CHARACTERISTICS:
LENTH: 4770 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAMB/KEY: CDS
LOCATION: 1..4761
SEQUENCE DESCRIPTION: SEQ ID NO: 45:
                                                                          LOCATION: 1..4761

SEQUENCE DESCRIPTION: SEQ ID NO: 45:

US-10-011-749-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 45, Application US/09000004
Patent No. 6780603
GENERAL INFORMATION:
        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                 487 GCAAACAATACAATGG 502
                                                                                                                                                                                                                                                           5 GCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington STATE: D.C.
                                                                        NAME/KEY: CDS
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US-09-000-004-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
STREET: 3000 K Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                               Query Match
Pest Local Similarity 93.8%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONDUTEY: U.S.A.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
MEDIUM TYPE: Floppy disk.
MEDIUM TYPE: Floppy disk.
MEDIUM TYPE: PC_OMPAILIBLE
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749

FILING DATE: 11-Dec-2001
CLASSIFICATION NUMBER: US/998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 27-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAMM: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELERPHONE: 0202,672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/10011749

Patent No. 6726912

GENERAL INFORMATION:
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
MCMILLAN, Nigel Alan John
WILLIAMS, Margaret Bridget
                                                                                                                                                           ; NAME/KEY: CDS
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-000-094-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 45:
               INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGHH: 4770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                487 GCAAACAATACAATGG 502
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TOPOLOGY: 1ii
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                                                                                          Gaps
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                                         72.0%; Score 14.4; DB 4; Length 4770; 93.8%; Pred. No. 4.8e+02; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                               Sequence 2, Application US/09521526
Patent No. 6290965
GENERAL INFORMATION:
APPLICANT: APPRICANT: HOFMANN, KATHRIN U.
APPLICANT: HOFMANN, KATHRIN U.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE
TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
72.0%; Score 14.4; DB 3; Length 8010;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application PC/TUS9511859
GENERAL INFORMATION:
APPLICANT: JANSEN, KATHRIN U.
APPLICANT: HOFMAIN, KATHRYN J.
TITLE OF INVENTION: DNA ENCODING HUMAN PAPILLOMA VIRUS TYPE
TITLE OF INVENTION: 6A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/521,526
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,468
FILING DATE: 22-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 19307
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
TELEPHONE: (908) 594-6734
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8010 base pairs
TYPE: mucleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIF: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3096 GCAAACAATACAATGG 3111
                                                                                                                                                                    487 GCAAACAATACAATGG 502
                                                                                                                               5 GCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GCAAACAGTACAATGG 20
                                     Query Match
Best Local Similarity 93.8°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
US-09-000-004-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCT-US95-11859-2
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APPLICANT: Blattner, Frederick R.
Burland, Valerie
Burland, Nicole T.
Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723e1 Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 72.0%; Score 14.4; DB 5; Length 8010; Best Local Similarity 93.8%; Pred. No. 5e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US

ZIP: 53701-2113

COMPUTER: READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Word Perfect 8.0

CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: «Unknown»
                                                                  CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEADELIN PC compatible
COMPUTER: BEADELIN PC compatible
COMPUTER: PATENTIN PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11859
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE - P.O. BOX 2000
CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,468
FILING DATE: 22-SEP-1994
ATTONNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 19307 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-6734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 47
US-09-453-702B-240
; Sequence 240, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3096 GCAAACAATACAATGG 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GCAAACAGTACAATGG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 8010 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WI
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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Gaps
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              Query Match 72.0%; Score 14.4; DB 4; Length 1830121; Best Local Similarity 93.8%; Pred. No. 3.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.0%; Score 14.4; DB 4; Length 1830121; 93.8%; Pred. No. 3.3e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20850
COMPUTER READBLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER. Dell Pentium
OPERAING SYSTEM: MS DOS v6.22
SOFTWAREN ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION NUMBER: US/429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-06-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
RETERENCE/OCKET NUMBER: PB186FICI
TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
"""""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
TOPOLOGY: linear
;
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1568257 Grcdchacarracaa 1568272
                                                                                                                                      1568257 GrcGcaaacarracaa 1568272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 50
US-10-329-960-1
; Sequence 1, Application US/10329960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville,
STATE: MD
COUNTRY: USA
                                                                                                                                    g
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US-09-557-884-1
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: the Nucleotide sequence of
; TITLE OF INVENTION: the Amemophilus influence of
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.0%; Score 14.4; DB 3; Length 10236; Best Local Similarity 93.8%; Pred. No. 5.1e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockwille
                                                                         NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECONGUNICATION INFORMATION:
TELEPHONE: (608) 251-5060
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 10236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,91
RELEPRENCE/DOCKET NUMBER: 9186P3
TELECONTUNICATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 240:
US-09-453-702B-240
                    APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  875 CGCAAACATTACAATG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CGCAAACAGTACAATG 19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-557-884-1
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FEATURE:
NAME/KEY: misc feature
LOCATION: (105121)...(105121)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc feature
LOCATION: (107248)...(107248)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (121344)...(121344)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (55569)..(55369)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (51602)..(51602)
DTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (65309). (65309)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWE/KEY: misc feature
LOCATION: (117<u>1</u>36)..(117136)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (120038)..(120038)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g or
                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a, t, g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a,
                          NAME/KEY: misc_feature
LOCATION: (47036)...(47036)
OTHER INFORMATION: n equals a,
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
LOCATION: (51805)..(51805)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals a,
                                                                                                                        NAME/KEY: misc feature
LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
MANE/KEY: misc_feature
LOCATION: (65313) ..(65313)
OTHER_INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals &
FEATURE:
GENERAL INFORMATION:
GENERAL INFORMATION:
FIGUREAL INFORMATION:
TITLE OF INVENTION: Nuclectide Sequence of the Haemophilus influenzae Rd Genome, Frage Patent No. 6742927
TITLE OF INVENTION: Nuclectide Sequence of the Haemophilus influenzae Rd Genome, Frage Patent No. 6742927
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186F1
CURRENT APPLICATION NUMBER: US/043,990
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 1095-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
LENGTH: 1830121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a, t, g or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (45593)..(45593)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEX: misc feature
LOCATION: (9921). (9921)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (40808)..(40810)
JTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FPATURE:
NAME/KEX: misc_feature
LOCATION: (44416)..(44416)
JTHER INFORMATION: n equals a, t, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (44905)..(44905)
DTHER INFORMATION: n equals a, t, g or
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals a, t, g
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MAME/KEY: misc feature
LOCATION: (29298): (29298)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc feature
LOCATION: (44975)...(44975)
OTHER INFORMATION: n equals a, t,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (122167)...(122167)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (122336)...(122336)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131340)...(131340)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (131360)...(131360)
OTHER INFORMATION: n equals a, t, g or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (139910)
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (139910)
OTHER INFORMATION: n equals a, t, g or c
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LOCATION: (140398)...(140398)
OTHER INFORMATION: n equals a, t, g or c
OTHER INFORMATION: n equals a, t, g or c
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NAME/KEY: misc_feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals a, t, g or
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LOCATION: (145171)..(145171)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (147197)..(147197).
OTHER INFORMATION: n equals a, t, g
FEATURE:
NAME/KEY: misc_feature
LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a, t, g
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LOCATION: (145942)
OTHER_INFORMATION: n equals a, t,
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Query Match 72.0%; Score 14.4; DB 4; Length 1830121; Best Local Similarity 93.8%; Pred. No. 3.3e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Search completed: December 3, 2004, 05:52:13 Job time : 112.316 secs

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CK880588 SGP140896 CA257189 SCGFL419 CF108675 Shultzomi CC571629 CH240_447 CE315639 Ligr-gss- CK63826 AA0805A12- AJ769685 AJ769685 BJ38122 603516050 CB307086 HFIGO71 H CC950585 BOLCY23TR	BM423010 DB3 Dieth CA05567 ssalrgb51 CA59997 wawlc.pko BH352493 CH230-330 AW421025 fj90904.x BU359829 603977886 BB667911 BB667911 CC590141 DG2-41a5	AC02108 RDG F AC	BW272985 BW272985 CA172398 SCSGSB100 BJ628974 BU5628974 CD833593 BN40.0670 BW944457 UI-M.EHOP BU75922 UI-M.EHOP BU75922 UI-R.PF00- CL541753 OB. Ba005 CK840545 UI-R.AF0- BU051324 1111041G0 BZ035563 cef84106. BZ035563 cef84106. BZ035563 cef84106. BZ035563 Cef84106. BZ035563 Cef84106. BZ035563 Cef84106. BZ035563 Cef84106. BZ035563 Cef84106. BZ035563 Cef84106.	BB002558 BB003059 BB003029 CK003375 CK003375 B16764 B16764 B4367.TVB CAZ196667 SPL017 BQ703270 UT-R-FF0- AL691586 DKFZ2313K CN761561 DNAAA30C BG01992 CK063366 CC176609. CC1042557 CC104257 CC10425	CK97363 4104038 B CE749588 1104038 B EH431703 BOGHJ26TF CD634971 BN45.043M CE742517 tigr-gss- CE528276 tigr-gss-
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Contact: Soares, MB
Contact: Soares, MB
Condinated Laboratory for Computational Genomics
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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8256
Fax: 319 335 8265
Enail: bento-soares@ulowa.edu
The sequence contained an oligo-dT track that was present in the oligo-drouglectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Not1 site and the oligo-dT track served to identify it as a clone from the normalized ventricle at 15 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distibution: Glones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 223-300,
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /nctoe="Vector: pr7730-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-BJZ library is a subfracted library derived from the following tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc, tissues: heart, atrium at 15 dpc, ventricle at 15.6 dpc, dpc, AV canal at 15 dpc. For a detailed description of the library from which this clone was derived, please visit our web site at retest-engy ulowa-edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996) TAG_IIB-UI-R-BJZ
                                                                                                                                           EST 28-NOV-2000
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 395)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                         BF415163
UI-R-BJ2-bov-f-09-0-UI.sl UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bov-f-09-0-UI 3', mRNA sequence.
    Gaps
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   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
Rattus norvegicus
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                                                             162 AGACGCAAACAGTACAATG 180
                                  1 AGTCGCAAACAGTACAATG 19
                                                                                                                                                                                                        BF415163.1 GI:11403152
   Conservative
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Best Local Similarity 94.7
Matches 18; Conservative
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   18;
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   Matches
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PUBMED
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BF415163
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CG611837 OST297300

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BO199952 UF-R-001

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AZ18858 SP 1012 B

AZ18852 SP 1012 B

AZ18852 SP 1012 B

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CB750216 AMGNNUC:N
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OST297300
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RPCI-24-2
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Sattus, sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 339)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Ret Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Index
Unpublished (1998)
Other ESTs: TC5628
Charact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.4; DB 1; Length 339;
Pred. No. 4e+02;
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AZ166852
BQ199952
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AI075831
W81888
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clone="RPLDG37"
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BX630884
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AZ188568
AW242743
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CB750216
CD340621
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                   AZ698040
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AI237821.1 GI:3831327
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94.7%;
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Best Local Similarity
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AI237821
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G71 bp mRNA linear EST 05-MAR-2004
UI-R-BJ2-bov-f-09-0-UI.810 UI-R-BJ2 Rattus norvegicus cDNA clone
UI-R-BJ2-bov-f-09-0-UI 3', mRNA sequence.
CK883049
EST.
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Bento Soares Rattus sp. cDNA clone
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Rattus norvegicus (Norway rat)
Rattus norvegicus (Norway rat)
Rattus norvegicus (Sartus)
Rattus norvegicus
Rattus horazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. (bases 1 to 660)
Lee,N.H., Glocek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
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Rattus sp.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleost
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Gene Index
Gene Index
Unpublished (1998)
Other ESTB: TG56628
Contact: Lee, NH
The Institute for Genomic Research
9712, Nedical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3229
Fax: (301)-838-0208
Email: nhlee@tigr.org
Email: nhlee@tigr.org
Seq primer: M13-21.
Location/Qualifiers
...660 """rertus sp.""
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/db_xref="atrc (inhost):2036244"
/db_xref="taxon:10118"
/clone="RBRCN62"
       Mismatches
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                                                                                                                                                                                                                                                                                                                  EST224615 Normalized rat brain,
RBRCN62 3' end, mRNA sequence.
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/dov stage="datable:020.01" |
/dov stage
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 955
Fax: 319 335 955
Fax: 319 335 955
Fax: 319 335 955
Fax: 319 335 956
Fax: 319 335 966
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UI-R-DM1-ckc-i-03-0-UI.81 UI-R-DM1 Rattus norvegicus CDNA clone
UI-R-DM1-ckc-i-03-0-UI 3', mRNA sequence.
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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    .462
/organism="Rattus norvegicus"

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/strain="Sprague-Dawley"
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                                                                                                                             University of Iowa

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781: 319 335 8250

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Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
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/dlone="UI-R-B22-bov-f-09-01"
/lab_host="BH108 (Life Technologies)"
/clone="UI-R-B22-bov-f-09-01"
/clone="UI-R-B22-bov-f-09-01"
/clone="UI-R-B22"
/clone="UI-R-B22"
/clone="UI-R-B22"
/clone="Vector: pT7T3D-Pac (Pharmacia) with a modified
polyvinker; Site=1: Not 1; Site=2: Eco R1; The UI-R-B22
library is a subtracted library derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest.eng.ulowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Bukaryota, Metazoa, Echinocaa, Echinocida,
Echinocida, Euchinocidae, Echinocaa, Echinocida,
Strongylocentrotus.

I (Dases I to 714)

Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J, Davidson, E.H.
and Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources

L Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

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SP_1011_B2_H01_SP6E Strongylocentrouts purpuratus, purple sea
urchin, sperm genomic BAC library Strongylocentrotus purpuratus
genomic clone Plate=1011 Col=2 Row=P, genomic survey sequence.
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87.0%; Score 17.4; DB 7; Length 671;
Best Local Similarity 94.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 1; Indels C
                                                                     Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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|mol_type="mRNA"
|strain="Sprague-Dawley"
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Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                         COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammala; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 562)

Bunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Rislam,H., Longacree,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R., Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Longuert: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1M0224014R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0224014 R, genomic survey sequence.
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                                                                   Davidson, EH, Hood,
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0224 row: O column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
Contact: Cameron, RA, Davidson, EH, H Division of Biology 156-29
California Institute of Technology Pasadena California 91125, USA Tel: (626) 793-3047
Fax: (626) 793-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               714.
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/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0224014"
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Location/Qualifiers
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Location/Qualifiers
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Mus musculus
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CO640930 660 bp mRNA linear EST 23-JUL-2004 USDA-FP 109667 Adult Glassy-winged Sharpshooter Homalodisca coagulata cDNA clone WHHCO56_B12 5', mRNA sequence.
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| Tab host="nbilob-T1 phage resistant"
| Jab host="balls BBa"
| /dlone lib="0R BBa"
| /note="Vector:"pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                    CL764044
OR BBa0134L22.f OR BBa Oryza rufipogon genomic clone OR_BBa0134L22
5', genomic survey sequence.
CL764044
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                               Gaps
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Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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84.0%; Score 16.8; DB 9; Length 657;
Best Local Similarity 90.0%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                                      84.0%; Score 16.8; DB 6; Length 613; 90.0%; Pred. No. 8.5e+02; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMAP Project
Unpublished (2004)
Contact: No A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Buliding Room 303, Tucson, AZ 85721-0036,
Tal: 520 625 9555
Fax: 520 621 1259
Email: http://genome.arizona.edu
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BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0134 row: L column: 22
Seg primer: TAA TAC GAC TCA CTA TAG GG
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Location/Qualifiers
1. .657
/ organism="Oryza rufipogon"
/mol type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR BB80134122"
spleen, muscle, and kidney."
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CO640930.1 GI:50562424
EST.
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                                                                                                                                  18; Conservative
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Oryza rufipogon
                                                                                                       Best Local Similarity
Matches 18; Conserv
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                                                                              Query Match
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SOURCE
ORGANISM
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CO640930
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JOURNAL
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Concorpynchus mykiss
Concorpynchus mykiss
Concorpynchus mykiss
Concorpynchus mykiss
Concorpynchus mykiss
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Erotacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

I (bases 1 to 613)
Se Rexroad (C.E. 3rd, Lee, Y., Keele, J.W., Karamycheva, S., Brown, G., Koop, B., Gahr, S.A., Palti, Y. and Quackenbush, J.
Sequence analysis of a rainbow trout cDNA library and creation of a gente index
Contact: Rexroad CE
USDA, ARS, National Center for Cool and Cold Water Aquaculture
11876 Leetown Road, Kearneysville, WW 25430, USA
Tel: 304 724 8340 x2129
Fax: 304 725 0351
Email: crexroad@noccwa.ars.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified by cross match v0.990329.
Seq primer: AGCGGATAACAATTCACACAGGA.

Seq primer: AGCGGATAACAATTCACACAGGA.
                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pward (gil 4722114 [gb] AF129072.1], a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From brain, gill, liver,
                                /lab host="B. Coli strain XLIO-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UGGIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="IRT18K05_A_F03"
/tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 AGTGGCAAACAGTACAATAG 450
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Matches 18; Conserv
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/mol_type="makA"
/db_xref="taxon:197043"
/db_xref="taxon:197043"
/db_xref="taxon:197043"
/clone="WHHCOS6_E12"
/fess="Wixed population"
/tissue_type="Adult whole body"
/dev_srage="Adult whole body"
/dev_srage="Adult Glassy-winged Sharpshooter"
/lone lib="Adult Glassy-winged Sharpshooter"
/lone lib="Adult Glassy-winged Sharpshooter"
/lone="Westor: Paluescript II SK+; Site 1: EcoRI; Site 2:
Xhol; A high quality EST with at least 200 contiguous
bass at Trace Tuner score of 20 or better. Construction
by L Hunnicutt and PM DANG, USDA, ARS, U.S. Horticultural
Res. Lab, Ft.Pierce, FL, USA."
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodea; Echinoidea;
Echinoidea; Euechinodea; Echinoidea;
Ethinoidea; Euechinoidea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.

I (Bases I to 742)
Swartzell,S., Malairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
Wray,G.A., Ethenschn,C.A., Lehrach,H., Britten,R.J. Davidson,B.H.
and Hood,L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Droc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
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"Az Dp. UNA integration of the constructures of the constructu
Homalodisca coagulata (glassy-winged sharpshooter)
Homalodisca coagulata
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Membracoidea;
Cicadellidae; Cicadellinae; Homalodisca.

( tages I to 66)
Hunter, W. B., Bausher, M. G., Dang, P. M., Costa, H., Chaparro, J. X., Shatters, R. G. Jr., McKenzie, C. L. and Sinisterra, X. H.
Bxpressed Genes from Glassy-winged Sharpshooter, Homalodisca coagulata, (Hemiptera: Cicadellidae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2003)
Context: Wayne B. Hunter, Phat M. Dang, USDA, ARS
U.S. Horticultural Research Lab
USDA-ARS
COOI South Rock Road, Ft. Pierce, FL 34945, USA
Tel: (772) 462-5898, (772) 462-5940
Fax: (772) 462-5986
Email: Whunter@ushrl.ars.usda.gov, pdang@ushrl.ars.usda.gov
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Division of Biology 156-29
California Institute of Technology
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AZ186566.1 GI:8369744
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Matches 18; Conservative
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AZ186566/c
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Tel: (626) 793-3047

Fax: (626) 793-3047

Email: acameromicaltech.edu

Plate: 1007 row: I column: 23

Seq primer: SP6

Class: BAC ends

I. 742.

Location/Qualifiers

I. 742.

Amol type="genomic DNA"

Amol type="genomic BAC library"

Amole="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Found Department | Found Depar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="malanotic melanoma, high MDR"
/lab host="mblanotic melanoma, high MDR"
/lab host="mblanotic melanoma, high MDR"
/clone lib="NIH WGC_62"
/clone lib="NIH WGC_62"
/note="forgan: skin; Vector: pDNR-LIB (Clontech); site_1:
Stil (ggccgcctcggcc); Site_2: Stil (ggccattatggcc);
Double-stranded CDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCAGAGGCGAGGCGGCGCGATTATGGCC-3' and 3' adaptor
(where B = A, C, or G and N = A, C, or C, or T). Wacrage
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4251707"
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 AGTCGAAAACGGTACAATGG 70
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COMMENT
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BF573660
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Losses 1 to 801)

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

Lorect Submission

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Lorect Submission

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Lorect Submission

(E-mail:hattori@gsc.riken.jp, Vokohama, Kanagawa 230-0045, Japan

(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSNg01. For BAC

library availability, please contact Kuniya Abe (abe@rtc.riken.jp).

Tsukuba Institute, Desource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-288-36-9189, fax: 81-298-36-9199
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Oryza rufipogon
Dukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Ebbryophyta; Poaceae;
Ebrhartoideae; Oryzeae; Oryza.
I, Chaese; Lto Bl.)
Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
musculus molossinus DNA, clone:MSMg01-356P13.T7, genomic survey
                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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BAC end Sequences of Library MSMg01
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="mixture of kidney and spleen"
/clone_Iib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .801
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
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Local Similarity 90.0%; Pred. No. 8.7e+02;
Les 18; Conservative 0; Mismatches 2;
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                                                                GI:48164241
                                                                                                             Mus musculus molossinus
Mus musculus molossinus
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: EcoRI
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LIBRARY
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OMAP project
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AG466985.1
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R.Site 2
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Medazoa; Echinodeanata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Echinoidea; Echinoidea; Expongylocentrotuse.

E. (Dasses I to 776)
S. (Ansers I to 776)
S. (Ansers I to 776)
Wray, G.A., Mallace, J.C., Poustka, A.J., Livingston, B.T., and Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and additional resources
I. Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Strongylocentrotus purpuratus"
/nol type="gamone DNA"
/nol type="gamone DNA"
/nol type="gamone DNA"
/clone="plate=1001 Col=19 Row=C"
/clone="plate=1001 Col=19 Row=C"
/clone lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="organ: sperm; Vector: BACe3.6; BAC Clones in B-Coli
DH10B"
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                                                                                                                                                                                                                                                                                                                                                     AZ183531 1.0 SPGE Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic abc library Strongylocentrotus purpuratus genomic clone Plate=1001 Col=19 Row=C, genomic survey sequence.
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      contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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84.0%; Score 16.8; DB 8; Length 776;

Best Local Similarity 90.0%; Pred. No. 8.7e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0
                                                                                                             84.0%; Score 16.8; DB 2; Length 773; 90.0%; Pred. No. 8.7e+02; ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1001 row: C column: 19
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High quality sequence stop: 776.
Location/Qualifiers
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                                                                                                                                                                                                                                  592 AGTCACCAACAGTACAATGG 611
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                                                                                                                                                              18; Conservative
                                                                                                                  Query Match
Best Local Similarity
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AG466985/c
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PUBMED
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AUTHORS
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Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Xenopus; Silurana.

Xenopodinae; Meropus; Nepherson, J., Warren, W., Graves, T.,

Mardis, E. and Wilson, R.

A physical map of the xenopus tropicalis genome

A physical map of the xenopus tropicalis genome

Onpublished (2003)

Contact: Richard K Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submissions@watson wustl.edu

Insert Lenghis. 17500 Std Error: 0.00

Seq primer: Sp6 ATTTAGGTGACATARG

Class: BAC ends

Class: BAC ends
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BE779512
BE779512.1 GI:10200710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CL044667 1027 bp DNA linear GSS 31-DEC-2003 CH216-61K14_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-61K14, genomic survey sequence.
      /clone lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                 Indels
                                                                                                                                                      84.0%; Score 16.8; DB 9;
90.0%; Pred. No. 8.9e+02;
iive 0; Mismatches 2;
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/mol type="genomic DNA"
/strain="Nigerian frog"
/db_xref="caxon:8364"
/clone="CH216-61K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence start: 5
High quality sequence stop: 815.
Location/Qualifiers
1..1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                      Query Match
Best Local Similarity 90.0%
Matches 18; Conservative
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Best Local Similarity 90.03
Matches 18; Conservative
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CL044667
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AUTHORS
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BE779512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza rufipogon"
//organism="Oryza rufipogon"
//or type="genomic DNA"
//db Xref="taxon:4529"
//clone="OR_CBa0040B18"
//closue="OPE="Voung leaves"
//dev stage="2" week old seedlings"
//lab_host="DH10B T1 phage resistant"
//lab_host="DH10B T2 phage resistant"
//clone libs="QR_CBa"
//note="Vector: phaginant; site_1: HindIII; site_2: HindIII;
drk treated 36 hrs before harvest"
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                                                                               University of Arizona
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0040 row: B column: 18
Seg primer: G040 row: B column: 18
Seg primer: GCC TCA TTA GGC ACC CCA
Class: BAC ends.
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84.0%; Score 16.8; DB 9; Length 811;
Best Local Similarity 90.0%; Pred. No. 8.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels (
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Xenopus tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
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GSS.
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CL044783
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AQ525102

HS 5232 B2 D10 SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Flate=808 Col=20 Row=H, genomic survey sequence.

AQ525102.1 GI:4772422
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| Argument | A
                                  /dev_stage="3rd_instar_larva"
/dev_stage="3rd_instar_larva"
/clone_lib="Exelixis FlyTag ML01 pSport-Tag21"
/note="Organ: fat body; Vector: pSport1-Tag21; Site_1:
Not1; Site_2: Xho1; RNA was isolated from fat body from
3rd instar_larva challenged with gram+/- bacteria. cDNA
was oligodT primed."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Edopterrygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
1 (bases I to 438)
1 (bases I to 438)
Peterson, E. and Swimmer, C.
Exeliats Flyyrag EST Project CK01 Library
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EK.891 row: B column: 12
High quality sequence stop: 437.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                  Score 16.4; DB 7; Length 383;
Pred. No. 1.3e+03;
0; Mismatches 1; Indels
        /clone="EC23473"
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CO263634.1 GI:49149219
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Best Local Similarity 94.4%;
Matches 17; Conservative
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Matches 17; Conservative
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AQ525102
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CO263634/c
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1088)

1 (bases 1 to 1088)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 Dubblished (1999)

4 Dubblished (1999)

5 Contact: Robert Strausberg, Ph.D.

5 Email: Gapba-remail.nih.gov

7 Issue Procurement: ATCC

6 CDA Library Preparation: Life Technologies, Inc.

7 CDA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

7 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

8 DNA Sequencing by: Incyte Genomics, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

8 http://image.lln.gov

8 Plate: LLAM9614 row: g column: 15.

8 Location/Qualifiers
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Life
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Metazoa; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophila; Drosophila;

Chen,F., Lagueux,M., Cheung,L.M., Chong,A., Goldschmidt,S.,

Hussain,S., Laufer,A., Oliva,J., Park,C., Wong,M., Amundsen,C.,

Exclixis Flyrag SST Project Miol Library

Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="IMAGE." retinoblastoma"
/lab_hoge="type="retinoblastoma"
/lab_hoge="type="retinoblastoma"
/lab_hoge="type="retinoblastoma"
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EC.234 row: G column: 1
High quality sequence stop: 382.
Location/Qualifiers
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/organism="Drosophila melanogaster"
/mol type="mRNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 AGTCGCACATAGTACAATGG 561
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Best Local S:
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CO182638
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AUTHORS
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412 AGTCGCGAACAGTACAAT 395
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R54168.1 GI:816070
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3887
Email: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plates 808 row: H column: 20
Seg primer: SP6
Class: BAC ends
                                                                    Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 444)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Strigeldida; Schistosomatoidea; Schistosomatidae; Schistosoma.
(bases 1 to 457)
Verjoveki-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M., Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr., Kitajima,J.P., Adamson,R.E., Ashton,P.D., Bonaldo,M.F.,
Coulson, P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
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                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
|mol_type="genomic DNA"
|db xref="taxon:9606"
|/clone="plate=808 Col=20 Row=H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 444.
Location/Qualifiers
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EST.
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                          sapiens (human)
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Schistosoma mansoni
                                                   Homo sapiens
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Best Local Similarity
Matches 17; Conserv
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CD062819/c
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Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa.R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Gordrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.
Transcriptome analysis of the accelomate human parasite Schistosoma
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1MAGE:41828 5', mRNA sequence.
RS4168
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Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-14-3091-2186
Fax: +55-15-3091-2186

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 475)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioguimica
Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson,R.
The Washu-Merck EST Project
The Washu-Merck EST Project
Unpublished (1953)
Contract: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Eaxi: 324 286 1810
Insert Size: 1865
High quality sequence stops: 327 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Schistosoma mansoni"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 35 (2), 148-157 (2003)
22879926
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1..579
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/ Mol_type="MRNA"
/ Mol_type="MRNA"
/ Mol_type="MRNA"
/ Clone="E014672"
/ Clone="Borgan: fat larva"
/ Clone lib="Exelixis FlyTag ML01 pSport-Tag21"
/ Clone="Organ: fat body; Vector: pSport1-Tag21, Site 1:
/ Not; Site_2: Xho1; RNA was isolated from fat body From Not1; Site_2: Xho1; RNA was isolated from fat body From Not is nitar larva challenged with gram+/- bacteria. CDNA was oligodT primed."
                                                                                                                                                                                                                                                                                                      CO192867 579 bp mRNA linear EST 21-JUN-2004 EC34672.5prime Exelixis FlyTag ML01 pSport-Tag21 Drosophila melanogaster cDNA clone EC34672 5, mRNA sequence.
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Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bobtera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
I (bases 1 to 579)
Chen, F., Lagueux, M., Cheung, L.M., Chong, A., Goldschmidt, S.,
Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C.,
Exelixis Flyrage EST Project Miol Library
Unpublished (2004)
Contact: Stapleton, M.
                                                                                                                Gaps
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One Cyclotron Rd, Berkeley, CA 94720, USA
Exa: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EC.346 row: F column: 12
High quality sequence stop: 574.
Location/Qualifiers
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                                                                                                                Indels
                                                                     Score 16.4; DB 7;
Pred. No. 1.4e+03;
0; Mismatches 1;
    was oligodT primed."
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CO192867.1 GI:49004042
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AQ558513
AQ558513.1 GI:4918245
                                                                   82.0%;
ilarity 94.4%;
Conservative
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Homo sapiens
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Best Local Similarity
Matches 17; Conserva
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AQ558513/c
LOCUS
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C0192867
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /oranism="Drosophila melanogaster"
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/do Zref="taxon:727"
/do zref="taxon:727"
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/clone lib="Exelixis PlyTag MLO pSport-Tag21"
/note="Corgan: fat body, Vector: pSportl-Tag21; Site 1:
Not1; Site 2: Xho1; RNA was isolated from fat body From 3rd instar larva challenged with gram+/- bacteria. cDNA
IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1865 Std Error: 0.00 Seq primer: M13RP1 High quality sequence stop: 327. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen, F., Lagueux, M., Cheung, L.M., Chong, A., Goldschmidt, S., Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C., Orton, A., Shao, A., Platt, D. and Swimmer, C. Exelixis FlyTag EST Project ML01 Library
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One Cyclotron Rd, Berkeley, CA 94720, USA
Exas: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EC.259 row: D column: 5
High quality sequence stop: 475.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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mol type="mRNA"
db_xref="gdb:414369"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 AGTCACAAACAGTACAANG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGTCGCAAACAGTACAATG 19
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                                                                                                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Matches 17; Conser
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CO183546
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JOURNAL
COMMENT
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/organism="Xenopus laevis"
//organism="Xenopus laevis"
//mol_type="mRNA"
//mol_type="mRNA"
//dobse="IMAGE:7209189"
//issue_type="Pooled samples from 6 adult Xenopus testis"
//lone="IMAGE:7209189"
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//lone="InfluB TonA"
//lone="Organ: testis; Vector: pExpress-1; Site_1: EcoRV;
//note="Organ: testis from 6 adult male testis. CDNA
//note="Organ: testis from 6 adult male testis."
//note="Organ: testis from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 18-JUN-2004
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Not1; Site_2: Xho1; RNA was isolated from fat body from 3rd instar larva challenged with gram+/- bacteria. cDNA was oligodT primed."
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
Boytera; Endopteryota, Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 629)
Chen, F., Laqueux, M., Cheung, L.M., Chong, A., Goldschmidt, S.,
Hussain, S., Laufer, A., Oliva, J., Park, C., Wong, M., Amundsen, C.,
Exelixis Flyrag EST Project ML01 Library
Unpublished (2004)
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: EC.14 row: A column: 5
High quality sequence stop: 534.
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plate: LLAM15096 row: d column: 19
High quality sequence stop: 615.
Location/Qualifiers
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CO180321.1 GI:48953202
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Best Local Similarity 94.4<sup>§</sup>
Matches 17, Conservative
                                                                                                                                           1. .614
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1 (Dasea 1 to 614)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Upublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Gancer Genomics

National Cancer Institute, NIH

Bidg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-remail.nih.gov

Tissue Procurement: Igor B. Dawid

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Colne distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGENCOURT 19146459 NICHD_XGC_Te2 Xenopus laevis cDNA clone
IMAGE:7209189 5', mRNA sequence.
                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I tosaes 1 to Sal.
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Grgan: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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82.0%; Score 16.4; DB 8; Length 588;
Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 588.
Location/Qualifiers
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CK806306
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/ organism="Schistosoma mansoni"
/ mol_type="genomic DNA"
/ strain="Puerto Rico"
/ bxref="taxon:6183"
/ clone="sml-44Ks"
/ clone="sml-44Ks"
/ clone="taxon:6183"
/ clone=
                                                                                                   Use of end sequences from Schistosoma mansoni (Puerto Rico strain)
Sml BAC library for gene discovery and map construction
Unpublished (2001)
Other Sass sml-AELSTF
Contact: Najib M. EL-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Malvales, Malvaceae, Malvoideae, Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelaayed@tigr.org
Clones are derived from the Schistosoma mansoni (Puerto Rico) Sml
BAC library. For clone availability, please contact Dr. Najib
El-Sayed at TIGR (nelsayed@tigr.org) or Dr. Phillip LoVerde at
State University of New York, Buffalo, New York, USA
(loverde@buffalo.edu)
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Suo, J., Liang, X. and Xue, Y.
The construction of a cDNA library from the ovule of Gossypium hirsutum and its EST analysis
Unpublished (2002)
Contact: Suo J
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AJ513412 Gossypium hirsutum ovule first day the flower opens Gossypium hirsutum cDNA clone suo08h10r3, mRNA sequence.
AJ513412
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The Institute of Genetics and Developmental Biology CAS
Nanyitiao 3, Zhongguancun, Haidian, Beijing, 100080, China.
                                 Shetty,J., Simpson,A., Malek,J., Koo,H., LoVerde,P.T. and
El-Sayed,N.M.
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Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: gapbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CLOR distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov
Plate: LLAMILIZE row. b column: 20

High quality sequence stop: 641.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Schistosoma mansoni
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
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Best Local Similarity 94.4%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 1;
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Xenopus laevis
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata, Ditrysia;
Neoptera; Endopterygota; Lepidoptera; Glossata, Ditrysia;
Bombycoldae; Bombycidae; Bombyx.

I (bases 1 to 603)
S Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X., Ku,Q., Zhu,Z., Li,G., Pan,M., Li,C., Shen,Y., Hou,Y., Wu,Z., Li,G., Pan,M., Li,C., Shen,Y., Lan,X., Yuan,L., Yang,G., Li,G., Zhu,Y., Xu,M., Shen,W., Wu,D., Xiang,Z., Yu,J., Wang,J., Zhang,Q., Lai,G., Zhang,X., Li,G., Zhang,Z., Li,J., Zhang,Q., Lan,F., Fang,L., Li,Y., Wang,J., Ye,J., Wong,G.K.-S., Yang,M., Shi,J., Wu,Q., Li,C., Li,D., Sun,Y., Zhang,Z., Yang,Z., Yang,Y., Xi,Y., Qi,Q., Li,C., Li,D., Sun,Y., Zhang,Z., Yang,Z., Li,W.
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Neoptera; Endoptererygota; Lepidoptera; Glossata; Ditrysia;
Bombycidea; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Bombycidae; Danbycidae; Danbycidae; Danbycidae; Danbycidae; Chang, C., Ent., Chang, C., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, J., Yang, G., Wan, Z., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z., Yu, J., Wang, J., Wang, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2004)
Conteact: Yang Huan Ming
Conteact: Yang Huan Ming
Beijing Genomics Institute
Chinese Academy of Sciences
Beijing Airport Industrial Zone B6, Beijing 101300, P.R.China
Email: hyangalgtp.ac.cn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Cao,Y. A draft sequence for the genome of the domesticated silkworm (Bombyx mori)
                                                                                                            CK539992 603 bp mRNA linear EE
rswhb0 003251.y1 swh Bombyx mori cDNA, mRNA sequence.
CK5399<u>9</u>2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescript II SK(+)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="ovary"
/dev_stage="5th-instar day-3 larva"
/clone_lib="swh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                         Bombyx mori (domestic silkworm)
Bombyx mori
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Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="DaZhao(P50)"
/db_xref="taxon:7091"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
                                                                                                                                                                                                          CK539992.1 GI:4092446
337 GTCGCAAACAGTACAA 322
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Best Local Similarity 100.0
Matches 16; Conservative
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AUTHORS
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CK539992
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CK542039
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17000659025141 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
1800447012327 5', mRNA sequence.
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/clone_"Vector: pSport1; Site 1: Sal1; Site 2: Not1; Whole adult mosquitoes (mixed sex/frozen on liquid nitrogen.cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
                                                                                                                                                                                                             the flower opens" hirsutum ovule first day the flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L. Cenera Anopheles gambiae EST project Unpublished (2002)
Contact: Holt R.A.
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                          Query Match 82.0%; Score 16.4; DB 1; Length 1536; Best Local Similarity 94.4%; Pred. No. 1.5e+03; Matches 17; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 414;
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Anopheles gambiae
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80.0%; Score 16; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0;
                              1. .1536
/ Organism="Gossypium hirsutum"
//organism="RNA"
/ cultivar="Zhongmian12"
/ db xref="taxon:363"
/ clone="suc08h1073"
/ tissue_type="first day the flower
/ clone="lib="Gossypium hirsutum oropens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 w. Gude Dr., Rockville, MD 20850, USA Tel: 2404533151
Fax: 2404534580
Fax: 2404534580
Fax: DAULRA@celera.com
Plate: NUO10045ER row: O column: 06
Seg primer: M13 Reverse.
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/clone="19600447012327"
/dev_stage="Adult"
/lab_host="DH10b"
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  Location/Qualifiers
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1 (bases 1 to 414)
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753 bp DNA linear GSS 17-JUN-2003 CH240 423E19.TARBAC13P2 CHOR1-240 Bos taurus genomic clone CC541986 CC541986.1 GI:31860270 GSS 10-JUN-2003 GSS 10-JUN-2003
                                                                                                                                                                                                                                                                                         BH607285 658 bp DNA linear GSS 15-DEC-2001
BOGKF79TF BOGK Brassica oleracea genomic clone BOGKF79, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica oleracea
Brassica oleracea
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 698)
Town,(.D., van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BOGKF79TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovídae;
Bovinae; Bos.
1 (bases 1 to 753)
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3712"
/clone="BOGKF79"
/clone=lib="BOGK"
/clone=lib="BOGK"
/note="Wector: pH051; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into pH051 using BstXI linkers"
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Fax: 301-838-0208
Bax: 301-838-0208
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
I. c698
                                           80.0%; Score 16; DB 8; Length 616; 100.0%; Pred. No. 2.2e+03; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                         BH607285.1 GI:17859731
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                                                                                                                                                               37 CGCAAACAGTACAATG 22
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Best Local Similarity 100.
Matches 16; Conservative
                                                Query Match
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                     survey sequence.
BH607285
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Bos taurus
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CC541986/c
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BH607285/c
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Li,R., Li,H., Li,G., Su,J., Wang,X., Li,G., Zhang,Z., Li,J.,
Zhang,Q., Wei,N., Xu,J., Sun,H., Dong,L., Liu,D., Zhao,S., Zhao,X.,
Meng,Q., Wei,N., Xu,J., Sun,H., Dong,L., Liu,D., Zhao,S., Zhao,X.,
Yang,H., Shi,J., Wu,Q., Li,Y., Wang,J., Ye,J., Wong,G.K.-S.,
Huang,Y., Xi,Y., Qi,Q., He,D., Huang,H., Zhang,Z., Wang,Z.,
and Cao,Y.
A draft sequence for the genome of the domesticated silkworm
(Bombyx mori)
Unpublished (2004)
Contact: Yang Huan Ming
Beijing Genomics Institute
Chinese Academy of Sciences
Beijing Airport Industrial Zone B6, Beijing 101300, P.R.China
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BOGIC86TF BOGI Brassica oleracea genomic clone BOGIC86, genomic
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Brassica cleracea
Brassica cleracea
Brassica cleracea
Brassica, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Viridiplantae, Streptophyta; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
I (bases I to 61)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Other GSSs: BooftC86TR
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/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
genomic DNA inserted into PHOS1 using BstXI linkers"
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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Tel: 301-838-3523
Fax: 301-838-0208
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80.0%; Score 16; DB 7; Length 614;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovary"
/dev stage="5th-instar day-3 larva"
/clone lib="swh"
/note="Vector: pBluescript II SK(+)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Brassica oleracea"
/mol_type="genomic DNA"
/srrain="rol00DH3"
/db xrefe"taxon:3712"
/clone="BoGIC86"
                                                                                                                                                                                                                                                                                                                                                         /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="DaZhao(P50)"
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:7091"
/sex="female"
                                                                                                                                                                                                                                                                                      Email: hyang@igtp.ac.cn.
Location/Qualifiers
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BH459616
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BH459616/c
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/mol_type="mRNA"
/cultivar="developmentstage"
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FORWARD: CAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2004)
Contact: D. Tagu
INRA Rennes
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Best Local Similarity 100.
Matches 16; Conservative
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S Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geor, K., Kroll, M., Shvartsbeyn, A., Gebregeorgis, E., Niermali, D., de Jong, P. and Fraesr, C. M. Mouse BAC End Sequences from Library RPCI-24

L Unpublished (1999)

Other GSSs: RPCI-24-257H19-TV

Contact: Shaying Zhao

Department of Enkaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                     Email: whole@begsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaen as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
British column: 19
Seg primer: SP6
Class: BAC ends.
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Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Marra,M., de Jong,P., Keele,J.W. and Kappes,S.M.
Bovine BAC End Sequences from Library CHORI-240, PLATES 399 to 478
Unpublished (2003)
Other GSSs: CH204, 423E19.T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /_clone_llb="CHORI-240"
/note="Vector: pTARBACI.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                     Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada VSZ 4E6
Tel: 604-877-6085
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RPCI-24-257H19.TJ RPCI-24 Mus musculus genomic clone
RPCI-24-257H19, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_423E19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .753
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Mus musculus
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100.0%; Fre
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BH071204.1 GI:14890801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                       Fax: 604-877-6276
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Best Local Similarity
-haq 16; Conserve
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Hunter, W., Martinez-Torres, D., Rahbe, Y., Sabater-Munoz, B.,
Stern, D., Tagu, D. and Wincker, P.
An expressed sequence tags database for the pea aphid Acyrthosiphon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Spleen/Brain"
/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using Mbo! partially digested male CS7BL/6J DNA."
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DDAAAASDHO9FM1 ApMS Acyrthosiphon pisum cDNA clone IDOAAA25DH09
5', mNA sequence.
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Tel: 301 838 0200
Fax: 301 838 0200
Examil: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC epage: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
Plate: 257 row: H column: 19
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Tel: +33.2.23.48.51.65
Fax: +33.2.23.48.51.50
Risk of contamination by bacterial sequences from obligatory
(Buchnera) or facultative endosymbionts. These sequences were
obtained in the frame of the International Consortium of Aphid
Genomics in collaboration with Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Pred. No. 2.3e+03;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 797
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
/clone="RPCI-24-257H19"
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Acyrthosiphon pisum
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Gaps

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Indels

DRIGIN

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Pred. No. 2.3e+03;
; Mismatches 0;
Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
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Homo sapiens
                                                                                                             3 TCGCAAACAGTACAAT
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/mol_type="mRNA"

/mol_type="mRNA"

/do_xref="taxon:7029"

/clone="wRAP031_C12"

/sex="Mixed population"

/tissue_type="whole body, nymphs and adults"

/tissue_type="whole body, nymphs adults"

/tissue_type="whol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B55 bp mRNA linear EST 04-MAY-2004 USDA-FP 129969 Acyrthosiphon pisum, Pea Aphid Acyrthosiphon pisum CN586897 CL2, mRNA sequence. CN586897.1 GI:46998620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                              /clone_libe="Application" / Clone_libe="Application" / Clone="Voctor: pBS-SK minus; Site 1: EcoRI; Site 2: XhoI; Sample name: ID0AAA; Plant growth place: Department of Ecology & Evolutionary Biology, Princeton University; Soil conditions: Soil; Sowing date: 01/06/1999; Princeton date: no stress; Harvestiption: Applias incoulated on one-week old Vicia faba under non-sterile conditions. All parthenogenetic stages and both winged and wingless adults were collected for library construction.; experimental condition: long photoperiod (16-hr light/8-hr dark at 18 c)"
                                                                           /tissue type="whole insect"
/dev stage="nymphs and adults (parthenogenetic females)"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hunter, W.B., Dang, P.M., Stern, D. and Lapointe, S.L.

Gene expression in Acyrthosiphon pisum (Hemiptera: Aphididae)

L. Unpublished (2004)

Contact: Mayne Hunter; Phat Dang
US. Horticultural Research Lab, Ft. Pierce, FL

2001 South Rock Rd, Ft. Pierce, FL 34945, USA

Tel: (772) 462-5898, (772) 462-5940

Fax: (772) 462-5986

Email: Whunterwoodshrl.ars.usda.gov.

Location/Qualifiers

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Acyrthosiphon pisum
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
Aphidoidea; Aphididae, Macrosiphini; Acyrthosiphon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80.0%; Score 16; DB 7; Length 827; 100.0%; Pred. No. 2.3e+03; ive 0; Mismatches 0; Indels
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Query Match

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/organism="Homo sapiens"
// Mod_Itype="mRNN"
// Mod_Itype="mRNN"
// Mod_Itype="mRNN"
// Lissue_Itype="germinal center B cell"
// Loone_Ithe="NOT_GGAP_GCB1"
// Clone_Ithe="NOT_GGAP_GCB1"
// Clone_Ithe="NOT_GGAP_GCB1"
// Clone_Ithe="NOT_GGAP_GCB1"
// Clone_Ither; Site_1: NOT I; Site_2: Eco RI; lst strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CESR). CDNA synthesis was primed with a Not I - oligo(dT) primer
// Startanded cDNA was ligated to Eco RI adaptors // Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
9/ Dp mENA linear EST 08-FEB-1998 similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
AA767086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CRSP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Scares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trace considered overall poor quality Insert Length: 1049 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGTCGCAAACAGTACAATG 19
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us-10-050-189a-7.rst

DEFINITION

RESULT 42 AI875704

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

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/notIte 1: PT773-Pac; Site 1: PT773-Pac; Site 1: PT773-Pac; Site 1: PT773-Pac; Site 1: PT773-Pac; Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 241)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                        Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 194)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Eno Ri site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbr/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                   NIH-WGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
Concact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 79.0%; Score 15.8; DB 2; Length 194; Local Similarity 89.5%; Pred. No. 2.6e+03; nes 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
IMAGE:3058467 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 AGCTGCAAACAGTACAATG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AGTCGCAAACAGTACAATG 19
                                AW404268
AW404268.1 GI:6923325
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                                                                                                                                                   Homo sapiens (human)
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .194
                                                                                                                                                                                                Homo sapiens
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                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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LOCUS
DEFINITION
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ORGANISM
                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
COMMENT
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TITLE
                                                                                                                                                                                                                                                                                                      REFERENCE
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KEYWORDS
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/note="Organ: kidney; Vector: pME186FE13; Site_1: DraIII
(CACTGTGG1); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGGGCCTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG]. KhoI should
be used to isolate the CNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sunio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Bases I to 152)

En I (Bases I to 152)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Ritter, E., Koha, Wilson, R., Yackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Other ESTS: uk51607.yl
Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLML; contact the IMAGE Consortium (infc@image.llnl.gov) for further information.
                                                                                                                                   AI875704 152 bp mRNA linear EST 21-JUL-1999 uk51£07.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1972549 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing: 5' end primer CTF primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .152
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
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/db_xref="taxon:10090"
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/sex="female"
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High quality sequence stop: 122.
Location/Qualifiers
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/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTAGCAAACACTACAATG 141
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EST.
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:989289
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source

FEATURES

LOCUS

RESULT 43 AW404268/c

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ORIGIN

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Gaps .. 0 EST 11-SEP-1998

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/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME188-FL3; Site_1: DraIII
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was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [IGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGATAAGGTGCG and 3' end
primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Strongylocentrotus purpuratus"
//nollype="genomic DNA"
//nollype="genomic DNA"
//nolloce="plate="1019" Coll-14"
//clone="lb="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
//note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 30-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea;
Echinoidea; Buechinoidea: Echinocea; Echinoida;
Strongylocentrotus.

1 (bases 1 to 294)
Cameron.R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H., and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ191734 SPEE Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1019 Col=14 Row=N, genomic survey sequence. AZ191734 GI:8374913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%; Score 15.8; DB 1; Length 241; 89.5%; Pred. No. 2.6e+03; ive 0; Mismatches 2; Indels C
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Division of Biology 156-29
California Institute of Technology
Pasadana California 91125, USA
Tel: (626) 395-8821
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 1019 row: N column: 14
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 294.
Location/Qualifiers
1. .294
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AGTAGCAAACACTACAATG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AGTCGCAAACAGTACAATG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
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KEYWORDS
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                                                                                                                          /...*Hemo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/do_type="mRNA"

/do_tyte="mRNA"

/dev_stage="two placentae: one from 8 weeks and another from 9 weeks post conception"

/do_top="byte="byte="proceeding="two placentae"

/do_top="byte="byte="proceding="two placentae"

/do_top="byte=
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Entaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dasses 1 to 241)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, T., Jackson, Y., Cardenas, M., McCann, R.,
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
Washington University School of Medicine
Fax: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI649302 241 bp mRNA linear EST 30-APR-1999 uk30d09.xI Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:1970513 3', mRNA sequence.
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This clone was previously sequenced on the 5' end only, this new data is from the 3' end data is from the 3' end Seq primer: custom primer used Seq primer: custom primer used High quality sequence stop: 112.

Location/Qualifiers
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       Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:1970513"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGTGGCAAACAGCACAATG 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI649302
AI649302.1 GI:4730136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.5
Matches 17; Conservative
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AI649302
LOCUS
DEFINITION
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AUTHORS
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ð g us-10-050-189a-7.rst

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

LOCUS

RESULT 47

g

A1434235

```
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
Insert Length: 1361 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 138.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab host="DH10B"
/clone lib="NCI_CGAP_Lym12"
/note="Organ: lymph node; Vector: pCMV-SPORT6; Site 1:
Sall; Site_2: Not!, Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             var. neoformans)
Cryttcocccus neoformans var. neoformans
Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (Lase, 1 to 303) NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: juneann-murphy@ouhsc.edu
This clone is available from the Fungal Genetics Stock Center,
Phone 913-588-7044, http://www.fgsc.net/ Contact Dr. Bruce Roe
(broe@ou.edu, www.genome.ou.edu) for sequencing questions Contact
Dr. Juneann Murphy(juneann-murphy@ouhsc.edu) for library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 bp mRNA linear EST 08-AUG-2 hieoform: strain B3501 Cryptococcus neoformans strain B3501 Cryptococcus neoformans commons var. neoformans cDNA clone hieofoiz 5', mRNA sequence. CF185222.1 GI:33507090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Filobasidiella.

1 (bases 1 to 307)

Kupfer, D.W., Drabenstot, S.D., Buchanan, K.L., Lai, H., Dyer, D.W.,
Roe, B.A. and Murphy, J.W.
Comparison of highly conserved intronic and exonic elements
associated with splicing among five diverse fungal organisms
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%; Score 15.8; DB 1; Length 303; 89.5%; Pred. No. 2.7e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Department of Microbiology and Immunology
University of Oklahoma Health Sciences Center
Oklahoma City, OK 73190, USA
Tel: 405-271-2133 ex2133
Email: juneann-murphy@ouhsc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/dorse="taxon:9606"
/clone="taxon:120882"
/tissue_type="lymphoma, fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 AGCTGCAAACAGTACAATG 262
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  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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TITLE
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Matches
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                                                                                                                                                                                                                                                                                            297 bp mRNA linear EST 30-MAR-1999 ti33b08.x1 NCI CGAP Lyml2 Homo sapiens cDNA clone IMAGE:2132247 3' similar to TR:Q12912 Q12912 LYMPHOID-RESTRICTED MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
www-bio.llhi.gov/bbrp//mage/image.html
Insert Length: 2729 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 175.
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/note="Organ: lymph node: Vector: pCNV-SPORT6; Site_1:
Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
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NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="lymphoma, follicular mixed small and large
                                                                          Gaps
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Pred. No. 2.7e+03;
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Contact: Robert Strausberg, Ph.D.

Email: gapbs-remail.nih.gov

Tissue Procurement: Mark Raffeld, M.D.

Tissue Procurement: Mark Raffeld, M.D.

CDNA Library Preparation: Stratagene, Inc.

CDNA Library Arrayed by: Greg Leanon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1396 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 273.

Location/Qualifiers
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Dijoo dr. Average insert size 0:8 kb. Non-amplified
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adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTTTTT 3'"
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1 (bases 1 to 324)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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79.0%; Score 15.8; DB 6; Length 307;
Best Local Similarity 89.5%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels
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High quality sequence stop: 296.
Location/Qualifiers
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Score 15.8; DB 1; Length 324; Pred. No. 2.7e+03;

79.0%; 89.5%;

Query Match Best Local Similarity

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        Matches
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        Conservative
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        Mismatches
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        Indels
        0;
        Gaps

        QY
        1 AGTGGCAACAGTACAATG
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        Db
        244 AGCTGCAACAGTACAATG
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Search completed: December 3, 2004, 05:48:27 Job time: 2612.05 secs

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Run ĕ

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3 AAA81520 3 AAA81520 4 ABL03868 3 AAA81514 3 AAA81528	3 AAA81528 12 ADM43182 6 ABQ76121 5 AAC88884	6 ABT08275 12 ADH23244 12 ADM43171	3 AAA81454 3 AAA81518 6 bbwcc220	3 AAA81453 3 AAA81453	3 AAA81489 8 3 AAA81490 14	3 AAA81490_14 2 AAZ06831	4 ABL07876 10 ADC00831	3 AAA81495 6 AAS20000	12 ADJ12457 3 AAA81456	3 AAA81456 3 AAA81465	3 AAA81501 3 AAA81501	3 AAA81457 3 AAA81457	10 ADC00365 3 AAA81458	3 AAA81458 3 AAA81487	3 AAA81487 3 AAA81478	3 AAA81478 3 AAA81476	3 AAA81476 3 AAA81459	AAA81459 AAA81469	10 ABS56454_21 4 AAF28546	3 AAA81502 3 AAA81479	3 AAA81479 6 AAL41152	3 AAA81468 3 AAA81468	3 AAA81463	10 ADC85287	9 ADA02807 10 ADB72545	12 ADM74402	3 AAF22293	AAA8146 AAA8146	AAT5884	AAZ0142	AAA8149	AAA8143	3 AAA81490 02 3 AAA81490 02 3 AAA81490 03
30078 31562 33303 33962	333962 34775 34793 34794	34794 34794 34796	35042	36471	37096	37668 37948	37996	44608 44861	45774 46593	46593 47475	48275	49646 49646	49650 49767	49767 50925	50925 52253	52253 56485	56485 56609	56609	62598 63563	65632 69936	69936 70768	72750	78845	96596	96597	96597	101786	102634 102634	110000	110000	110000	110000	1100000 1100000 1100000
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Aaa97179 Oligonucl
Aaa08325 ICAM-R mu
Aac91958 Human ICA
Abk09368 Monoclona
Adq25757 Human ICA
Ach00956 Human pap
Ach00956 Human pap
Ach01756 Enterchae
Aba50762 Human spl
Aba50762 Human spl
Aba60139 Probe #13
Aba68320 Human foe
Aai4834 Probe #13
Aba68320 Human ben
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Aba50367 Human ben
Aai4835 Human ben
Aai6859 Human ben
Aba16859 Human ben
Aba16859 Probe #13
Aba66250 Human ben
Aba16859 Probe #11
Aai0859 Probe #11
Aai0855 Human ben
Aai46437 Human ben
Aai46431 Human ben
Aai1169 Probe #11
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Aai0856 Human ben
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Aak40411 Human ben
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ACH00956
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ABS16511
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ABS42073
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The invention provides a method for detecting a polymorphism linked to a gene associated with familial dysautonomia (FD). This involves detecting a disruptive mutation in a gene encoding the IkappaB kinase-complex.

a sociated protein (IKAP) on chromosome gdil. StappaB kinase-complex.

C Examilito in position of the donor splice site of intron 20.

This mutation (2507+6T to C) results in the generation of an IKAP mRNA in which exon 20 is spliced out along with intron 20. Sequence analysis of the IKAP gene of individuals heteroxygous for the FO foromosome with the most common minor haplotype (minor 2) showed a G to C transversion of not succeed in a splice of interpretation of a consensus Ser/Thr of succeeding usbetitution and disruption of a consensus Ser/Thr kinase phosphorylation site. The present sequence is a primer that can be used in a claimed method for detecting a disruptive mutation in the IKAP consensus services in a claimed method for detecting a disruptive mutation in the IKAP consensus homosygous for the major soft in a family with the primer was used in the genotype analysis of FD alleles. Use with the probands homosygous for the major haplotype, all affected individuals content and the proband were heteroxygous for the major and minor 2 FD content and the proband were heteroxygous for the major for the major for the major for the major for the probands were homozygous for the major for the major for the probands were heteroxygous for the major for the major for the probands were heteroxygous for the major for the probands were heteroxygous for the major for c mutation. Study content probands were homozygous for the major for pakenasi descent revealed the presence of 25 carriers of 2507+6T to C and 2 individuals with R096P content presence of 25 carriers of 2507+6T to C and 2 individuals with R096P content in the presence of 25 carriers of 2507+6T to C and 2 individuals with R096P contents were deteroxygous for the presence of 25 carriers of 2507+6T to C and 2 individuals with probands were detero

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Human; IKBKAP; Familial Dysautonomia; FD; Riley-Day syndrome;
Hereditary Sensory and Autonomic Neuropathy Type III; carrier screening;
FD2; mutation; gene; chromosome 9q31; ds.
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